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<110>   Renz, Andreas
        Sozer, Nursen
        Frentzen, Margit
        Bauer, Jorg
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        Abbadi, Amine
        Heinz, Ernst

<120>   NOVEL PLANT ACYLTRANSFERASES SPECIFIC FOR LONG-CHAINED, MULTIPLY
        UNSATURATED FATTY ACIDS

<130>   13478-00002-US

<150>   PCT/EP2004/003224
<151>   2004-03-26

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Ala Lys Thr Ala Val Gly Leu Leu Thr Leu Ala Pro Ala Arg Ile Val
            10              15              20
ttc ctc gtg act gtc ctg ggc acg tac ggg ctc acg gtc gcg gcc tgc       151
Phe Leu Val Thr Val Leu Gly Thr Tyr Gly Leu Thr Val Ala Ala Cys
        25              30              35
acg cga ctt ggc gtc ccg aaa agc ttc gtg ctg ggc ctg acg cgg tgc       199
Thr Arg Leu Gly Val Pro Lys Ser Phe Val Leu Gly Leu Thr Arg Cys
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gtc gcg cga ctc acg ctc tgg ggg ctt ggg ttc tac cac att gag gtc       247
Val Ala Arg Leu Thr Leu Trp Gly Leu Gly Phe Tyr His Ile Glu Val
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                      75                    80                   85
aac cac gtc tcg tac ctg gag atc ttg tac ttc atg tcg acc gtg cac      343
Asn His Val Ser Tyr Leu Glu Ile Leu Tyr Phe Met Ser Thr Val His
                      90                    95                  100
tgc ccg tct ttc gtc atg aag aag acc tgc ctc cga gtc ccg ctt gtc      391
Cys Pro Ser Phe Val Met Lys Lys Thr Cys Leu Arg Val Pro Leu Val
         105                   110                  115
ggc tac att gcc atg gag ctg ggc ggt gtg att gtg gac cgc gag ggc      439
Gly Tyr Ile Ala Met Glu Leu Gly Gly Val Ile Val Asp Arg Glu Gly
         120                   125                  130
ggc ggt caa agc gca tcg gcg atc att cgc gac cgc gtg cag gag cct      487
Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg Asp Arg Val Gln Glu Pro
135                   140                  145                  150
cct cga gat tcg tcg agc gag aag cac cac gcg cag ccg ctt ctt gtg      535
Pro Arg Asp Ser Ser Ser Glu Lys His His Ala Gln Pro Leu Leu Val
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Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser Cys Leu Leu Gln Phe Lys
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acg gga gcc ttt cgt cct ggg gct ccg gtg ctt ccg gtc gtg ctt gag      631
Thr Gly Ala Phe Arg Pro Gly Ala Pro Val Leu Pro Val Val Leu Glu
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ttt ccg att gac aaa gcg cgt ggt gac ttt tcc ccg gcg tac gaa tcg      679
Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe Ser Pro Ala Tyr Glu Ser
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gtc cac acg cca gct cac ctc ctt cgc atg ctc gca caa tgg agg cac      727
Val His Thr Pro Ala His Leu Leu Arg Met Leu Ala Gln Trp Arg His
215                   220                  225                  230
cgg ctt cgg gtg cgc tat ctt cct ctg tat gag ccc tct gcg gct gag      775
Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr Glu Pro Ser Ala Ala Glu
                      235                  240                  245
aag gtt gat gca gac ctt tat gcg cgg aac gtg cgc gac gaa atg gcg      823
Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn Val Arg Asp Glu Met Ala
                      250                  255                  260
cgc gcg ctc aag gta ccc act gtg gag cag tct tac cgc gac aag ctc      871
Arg Ala Leu Lys Val Pro Thr Val Glu Gln Ser Tyr Arg Asp Lys Leu
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gtc tac cac gcg gat ctc atg ccg cac tac cag aag gcc ggc ccc gga      919
Val Tyr His Ala Asp Leu Met Pro His Tyr Gln Lys Ala Gly Pro Gly
         280                   285                  290
gcg ctc tat ctg tac gtc cga cct gac ctc ttg tagcactcat gcgcgtccca      972
Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu Leu
295                   300                  305
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Leu Thr Val Ala Ala Cys Thr Arg Leu Gly Val Pro Lys Ser Phe Val
        35                  40                  45
Leu Gly Leu Thr Arg Cys Val Ala Arg Leu Thr Leu Trp Gly Leu Gly
    50                  55                  60
Phe Tyr His Ile Glu Val Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp
65                  70                  75                  80
Pro Arg Val Ile Val Ala Asn His Val Ser Tyr Leu Glu Ile Leu Tyr
            85                  90                  95
Phe Met Ser Thr Val His Cys Pro Ser Phe Val Met Lys Lys Thr Cys
            100                 105                 110
Leu Arg Val Pro Leu Val Gly Tyr Ile Ala Met Glu Leu Gly Gly Val
        115                 120                 125
Ile Val Asp Arg Glu Gly Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg
    130                 135                 140
Asp Arg Val Gln Glu Pro Pro Arg Asp Ser Ser Ser Glu Lys His His
145                 150                 155                 160
Ala Gln Pro Leu Leu Val Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser
            165                 170                 175
Cys Leu Leu Gln Phe Lys Thr Gly Ala Phe Arg Pro Gly Ala Pro Val
        180                 185                 190
Leu Pro Val Val Leu Glu Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe
        195                 200                 205
Ser Pro Ala Tyr Glu Ser Val His Thr Pro Ala His Leu Leu Arg Met
    210                 215                 220
Leu Ala Gln Trp Arg His Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr
225                 230                 235                 240
Glu Pro Ser Ala Ala Glu Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn
            245                 250                 255
Val Arg Asp Glu Met Ala Arg Ala Leu Lys Val Pro Thr Val Glu Gln
            260                 265                 270
Ser Tyr Arg Asp Lys Leu Val Tyr His Ala Asp Leu Met Pro His Tyr
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Gln Lys Ala Gly Pro Gly Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu
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Leu
305


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<213>  Physcomitrella patens

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aactgaaaac ttgtttttaat tttttcttaa attgaaattc tgtgcctgaa agccaactct      180
aggtccatca taatgtagca atatgatcag aagcgctcaa atgtgtcgtg aaagtttgct      240
tttgcaattt tcttttgctg ttaacctatt gattatgttg gaaccacaat acagacgctg      300
cttcacttca ttcttatggc aatgaatgtc gtgatgattc cggttaattt catcctacag      360
ggatatggat gttgtaaagg tgattttttgc aggtgataaa gtacctaagg agaaccgtgt      420
gatggtcatg tgcaaccatc gtaccgaagt ggactggatg tacatttgga acttagcaat      480
tcggaaaggc aagattgggt actgcaagta tgcggtgaag aactcagtga aaaacttacc      540
cttgtttggt tgggcatttt acgttttttga gtttctgatg ctgcatagaa agtgggaagt      600
ggatgctccc gtcatcaaga catacattga cagttttcaa gataaaagag atcctctctg      660
gctagtcgtg tttcctgaag cacagatttt ttcgtaaggc tgaagtaccc atccatggct      720
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agtaaatcat acttgcttaa tgtacttagc aatttgtcat ttttgactta ttgtgatgta      840
aatgtgattg actactatga cagtgaagcg aaacgggaca cgggcaatgc aattggaaga      900
gagaaaggct atccggagct tgtcaatgtg cttcaacctc gcactcgtgg ctttgtgact      960
tgcctttctc aatcgcgctg ctctttggat gcagtttatg acctcactat agggtacaag     1020
aagcggtgtc ccttgttcat caacaatgta ttcggaaccg atccatcgga agtgcacatt     1080
cacattcgcc gaataccaat ttctgagatt cctcaatcag aagacggtat gacgcagtgg     1140
ctgtatgatc tattttatca aaaggaccag atgttggcca gtttttagtaa gacaggctct     1200
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1               5                   10                  15
tct gtt gtt tct cta gca agt aaa tca tac ttg ctt aat gta ctt agc       96
Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser
                20                  25                  30
aat ttg tca ttt ttg act tat tgt gat gta aat gtg att gac tac tat      144
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr
            35                  40                  45
gac agt gaa gcg aaa cgg gac acg ggc aat gca att gga aga gag aaa      192
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys
        50                  55                  60
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ggc tat ccg gag ctt gtc aat gtg ctt caa cct cgc act cgt ggc ttt        240
Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe
65              70                  75                  80
gtg act tgc ctt tct caa tcg cgc tgc tct ttg gat gca gtt tat gac        288
Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp
                85                  90                  95
ctc act ata ggg tac aag aag cgg tgt ccc ttg ttc atc aac aat gta        336
Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val
                100                 105                 110
ttc gga acc gat cca tcg gaa gtg cac att cac att cgc cga ata cca        384
Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro
                115                 120                 125
att tct gag att cct caa tca gaa gac ggt atg acg cag tgg ctg tat        432
Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr
        130                 135                 140
gat cta ttt tat caa aag gac cag atg ttg gcc agt ttt agt aag aca        480
Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr
145                 150                 155                 160
ggc tct ttc cct gac agt gga att gaa gag agc cct ttg aac ata gtg        528
Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val
                165                 170                 175
gaa ggt gtt tgc aat gtt gct cta cac gta gtc ctt agc ggt tgg gta        576
Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val
                180                 185                 190
ttc tgg tgc ttg ttt cat tcg gtt tgg ttg aag ctt tat gtg gct ttc        624
Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe
                195                 200                 205
gct agt ttg ctg ctc gcg ttt agt acc tat ttt gat tgg aga cct aaa        672
Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys
        210                 215                 220
ccg gtt tac tct agt cta cgt act aaa aga aaa atc gtg taa              714
Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val
225                 230                 235
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Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr
                35                  40                  45
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys
        50                  55                  60
Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe
65                  70                  75                  80
Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp
                85                  90                  95
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Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val
        100                 105                 110
Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro
        115                 120                 125
Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr
        130                 135                 140
Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr
145                 150                 155                 160
Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val
                165                 170                 175
Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val
            180                 185                 190
Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe
        195                 200                 205
Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys
210                 215                 220
Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val
225                 230                 235
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<213>  Physcomitrella patens

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acaatatgtg gtcccacgtc atgttgttcc cggagggcac taccaccaat ggcagagcaa    180
taatcgcctt caaaacagga gcattttcgc ctggtctccc tgtgcagcca atggttatta    240
gataccctca caagtatgtc aacccctctt ggtgtgacca aggaggtccg ttggtcgttg    300
tgttgcagct gatgactcag ttcatcaacc acatggaggt tgaatatttg ccggtcatga    360
agccaactgt gagagagatg aaataccctc atgaattcgc aagtagagtt cgcagcgaga    420
tggctaaagc gttaggcatc gtgtgcacag aacacagctt tctggatatt aagctagcgc    480
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<211>  1566

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ctc aac ggg ctc gaa acg cca cta ctg gct gaa ttt cct ctt ggc gaa      96
Leu Asn Gly Leu Glu Thr Pro Leu Leu Ala Glu Phe Pro Leu Gly Glu
                20                  25                  30
cgg cct aca ata ggg ccg gag gca cca gta aat ccc ttc cat gaa ccc     144
Arg Pro Thr Ile Gly Pro Glu Ala Pro Val Asn Pro Phe His Glu Pro
            35                  40                  45
gat ggt ggt tgg aag acc aac aac gag tgg aat tac ttt caa atg atg     192
Asp Gly Gly Trp Lys Thr Asn Asn Glu Trp Asn Tyr Phe Gln Met Met
        50                  55                  60
aaa tcc att ttg ctg att cca ctt ctt ctc gtt cgt cta gtg agc atg     240
Lys Ser Ile Leu Leu Ile Pro Leu Leu Leu Val Arg Leu Val Ser Met
65                  70                  75                  80
ata aca atc gta gca ttt gga tat gtg tgg atc agg att tgt ctg atc     288
Ile Thr Ile Val Ala Phe Gly Tyr Val Trp Ile Arg Ile Cys Leu Ile
                85                  90                  95
ggc gtc aca gat ccc ttg ttt aag cct ttc aat ccg tgt cga cgg ttc     336
Gly Val Thr Asp Pro Leu Phe Lys Pro Phe Asn Pro Cys Arg Arg Phe
            100                 105                 110
atg ctg tgg ggc ata cgg tta gta gca aga gca gtg atg ttt acc atg     384
Met Leu Trp Gly Ile Arg Leu Val Ala Arg Ala Val Met Phe Thr Met
            115                 120                 125
ggt tat tac tac att ccc atc aag gga aaa ccg gct cac cga tca gag     432
Gly Tyr Tyr Tyr Ile Pro Ile Lys Gly Lys Pro Ala His Arg Ser Glu
        130                 135                 140
gcg ccc att att gtg tcc aat cac att gga ttt ctg gat ccc atc ttt     480
Ala Pro Ile Ile Val Ser Asn His Ile Gly Phe Leu Asp Pro Ile Phe
145                 150                 155                 160
gtg ttc tat cgg cac ttg ccg gcc atc gtc tca gcc aag gag aac gtc     528
Val Phe Tyr Arg His Leu Pro Ala Ile Val Ser Ala Lys Glu Asn Val
                165                 170                 175
gag atg ccc att att gga ctg ttt ttg caa gct ttg caa ata ata ccc     576
Glu Met Pro Ile Ile Gly Leu Phe Leu Gln Ala Leu Gln Ile Ile Pro
            180                 185                 190
gtg gac cgg act gat gct cag tct agg cac cac gcg gct ggc aac gtt     624
Val Asp Arg Thr Asp Ala Gln Ser Arg His His Ala Ala Gly Asn Val
            195                 200                 205
cgg cga agg gct gtg gac aat atg tgg tcc cac gtc atg ttg ttc ccg     672
Arg Arg Arg Ala Val Asp Asn Met Trp Ser His Val Met Leu Phe Pro
        210                 215                 220
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Gln Gly Thr Thr Thr Asn Gly Arg Ala Ile Ile Ala Phe Lys Thr Gly
225                 230                 235                 240
gca ttt tcg cct ggt ctc cct gtg cag cca atg gtt att aga tac cct     768
Ala Phe Ser Pro Gly Leu Pro Val Gln Pro Met Val Ile Arg Tyr Pro
                245                 250                 255
cac aag tat gtc aac ccc tct tgg tgt gac caa gga ggt ccg ttg gtc     816
His Lys Tyr Val Asn Pro Ser Trp Cys Asp Gln Gly Gly Pro Leu Val
                260                 265                 270
gtt gtg ttg cag ctg atg act cag ttc atc aac cac atg gag gtt gaa     864
Val Val Leu Gln Leu Met Thr Gln Phe Ile Asn His Met Glu Val Glu
            275                 280                 285
tat ttg ccg gtc atg aag cca act gtg aga gag atg aaa tac cct cat     912
Tyr Leu Pro Val Met Lys Pro Thr Val Arg Glu Met Lys Tyr Pro His
        290                 295                 300
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gaa ttc gca agt aga gtt cgc agc gag atg gct aaa gcg tta ggc atc      960
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305                     310                 315                 320
gtg tgc aca gaa cac agc ttt ctg gat att aag cta gcg ctg gct gca     1008
Val Cys Thr Glu His Ser Phe Leu Asp Ile Lys Leu Ala Leu Ala Ala
                    325                 330                 335
gaa aag ctc aaa cag cct tca ggt cgg tcg ttg gtt gag ttt gct cgc     1056
Glu Lys Leu Lys Gln Pro Ser Gly Arg Ser Leu Val Glu Phe Ala Arg
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atg gag aag tta ttt cgg ctg gat ttt cct acg gcg aag gaa tac ttg     1104
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                370                 375                 380
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Glu Glu Leu Cys Thr Ala Leu Asp Leu Pro Arg Ser Pro Ile Thr Lys
385                     390                 395                 400
cag gtg ttc aac ctt ttc gat aag gat ggg cat gga agc ata aac ttt     1248
Gln Val Phe Asn Leu Phe Asp Lys Asp Gly His Gly Ser Ile Asn Phe
                    405                 410                 415
cga gag ttt ttg gca ggg ctc gcc ttt gtg tcc agc cac aca tca ttt     1296
Arg Glu Phe Leu Ala Gly Leu Ala Phe Val Ser Ser His Thr Ser Phe
                420                 425                 430
tca agt aca atg gag gct gca ttt aaa gca tgt gat gtg aat ggc gat     1344
Ser Ser Thr Met Glu Ala Ala Phe Lys Ala Cys Asp Val Asn Gly Asp
                435                 440                 445
ggc act ctt tct cgt gat gaa gtg gag agg agt ttg ctt gat atc ttt     1392
Gly Thr Leu Ser Arg Asp Glu Val Glu Arg Ser Leu Leu Asp Ile Phe
                450                 455                 460
cca gag ctc cct cca ata acg gtg ttc aag ctt ttt gac acg tta gat     1440
Pro Glu Leu Pro Pro Ile Thr Val Phe Lys Leu Phe Asp Thr Leu Asp
465                     470                 475                 480
ata aat cat gat gag aaa atc agc tgg gag gag ttc agt agc ttt ctg     1488
Ile Asn His Asp Glu Lys Ile Ser Trp Glu Glu Phe Ser Ser Phe Leu
                    485                 490                 495
cag cga aac cca gag tat ctg gcc atc att ata tat gcg cac cct act     1536
Gln Arg Asn Pro Glu Tyr Leu Ala Ile Ile Ile Tyr Ala His Pro Thr
                500                 505                 510
ctg ctg aag cca ccc aca tcg act agc tga                             1566
Leu Leu Lys Pro Pro Thr Ser Thr Ser
                515                 520
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<211>   521

<212>   PRT

<213>   Physcomitrella patens

<400>   8

Met Glu Ser Thr Ala Asp Val Gly Met Ser Asp Asp Asp Pro Ile Leu
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                20                  25                  30
Arg Pro Thr Ile Gly Pro Glu Ala Pro Val Asn Pro Phe His Glu Pro
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Asp Gly Gly Trp Lys Thr Asn Asn Glu Trp Asn Tyr Phe Gln Met Met
      50                      55                      60
Lys Ser Ile Leu Leu Ile Pro Leu Leu Leu Val Arg Leu Val Ser Met
65                      70                      75                      80
Ile Thr Ile Val Ala Phe Gly Tyr Val Trp Ile Arg Ile Cys Leu Ile
                  85                      90                      95
Gly Val Thr Asp Pro Leu Phe Lys Pro Phe Asn Pro Cys Arg Arg Phe
                  100                     105                     110
Met Leu Trp Gly Ile Arg Leu Val Ala Arg Ala Val Met Phe Thr Met
          115                     120                     125
Gly Tyr Tyr Tyr Ile Pro Ile Lys Gly Lys Pro Ala His Arg Ser Glu
      130                     135                     140
Ala Pro Ile Ile Val Ser Asn His Ile Gly Phe Leu Asp Pro Ile Phe
145                     150                     155                     160
Val Phe Tyr Arg His Leu Pro Ala Ile Val Ser Ala Lys Glu Asn Val
                  165                     170                     175
Glu Met Pro Ile Ile Gly Leu Phe Leu Gln Ala Leu Gln Ile Ile Pro
                  180                     185                     190
Val Asp Arg Thr Asp Ala Gln Ser Arg His His Ala Ala Gly Asn Val
                  195                     200                     205
Arg Arg Arg Ala Val Asp Asn Met Trp Ser His Val Met Leu Phe Pro
210                     215                     220
Gln Gly Thr Thr Thr Asn Gly Arg Ala Ile Ile Ala Phe Lys Thr Gly
225                     230                     235                     240
Ala Phe Ser Pro Gly Leu Pro Val Gln Pro Met Val Ile Arg Tyr Pro
                  245                     250                     255
His Lys Tyr Val Asn Pro Ser Trp Cys Asp Gln Gly Gly Pro Leu Val
              260                     265                     270
Val Val Leu Gln Leu Met Thr Gln Phe Ile Asn His Met Glu Val Glu
          275                   ·   280                     285
Tyr Leu Pro Val Met Lys Pro Thr Val Arg Glu Met Lys Tyr Pro His
          290                     295                     300
Glu Phe Ala Ser Arg Val Arg Ser Glu Met Ala Lys Ala Leu Gly Ile
305                     310                     315                     320
Val Cys Thr Glu His Ser Phe Leu Asp Ile Lys Leu Ala Leu Ala Ala
                  325                     330                     335
Glu Lys Leu Lys Gln Pro Ser Gly Arg Ser Leu Val Glu Phe Ala Arg
          340                     345                     350
Met Glu Lys Leu Phe Arg Leu Asp Phe Pro Thr Ala Lys Glu Tyr Leu
          355                     360 .                   365
Glu Lys Phe Ser Ala Met Asp Arg Thr His Ser Gly Phe Val Thr Phe
          370                     375                     380
Glu Glu Leu Cys Thr Ala Leu Asp Leu Pro Arg Ser Pro Ile Thr Lys
385                     390                     395                     400
Gln Val Phe Asn Leu Phe Asp Lys Asp Gly His Gly Ser Ile Asn Phe
                  405                     410                     415
Arg Glu Phe Leu Ala Gly Leu Ala Phe Val Ser Ser His Thr Ser Phe
              420                     425                     430
Ser Ser Thr Met Glu Ala Ala Phe Lys Ala Cys Asp Val Asn Gly Asp
          435                     440                     445
Gly Thr Leu Ser Arg Asp Glu Val Glu Arg Ser Leu Leu Asp Ile Phe
      450                     455                     460
Pro Glu Leu Pro Pro Ile Thr Val Phe Lys Leu Phe Asp Thr Leu Asp
465                     470                     475                     480
Ile Asn His Asp Glu Lys Ile Ser Trp Glu Glu Phe Ser Ser Phe Leu
                  485                     490                     495
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```
Gln Arg Asn Pro Glu Tyr Leu Ala Ile Ile Ile Tyr Ala His Pro Thr
            500                 505                 510
Leu Leu Lys Pro Pro Thr Ser Thr Ser
        515                 520


<210>  9

<211>  2217

<212>  DNA
<213>  Physcomitrella patens

<220>
<221>  CDS
<222>  (281)..(1837)
<223>  LPAAT2


<400>  9

ggcgcgccag aggacgagac aagggggggcg ctgtggactt ggtacaactc caaatgtggc      60
tctgaatcat caactaaggg tatggttata caaagtgcgt gccgccgaag agacagacct     120
tcttggttac ccaagactga atgaagatgg gaagtggaac gatagtatga tggctcagag     180
acgagtggct ccgagttttt tggtactcag taggaagttg caagtggggt ttgcatgctg     240
aagaatcgac actgcacagg cctcaccatc gacggatagc atg acc agc acg gaa      295
                                                  Met Thr Ser Thr Glu
                                                   1               5
aat act gcg atg ttc aca gaa gac act agc act cta aac ggc tcc aca      343
Asn Thr Ala Met Phe Thr Glu Asp Thr Ser Thr Leu Asn Gly Ser Thr
                10                  15                  20
gag gca aat cat gct gag ttt cct ctt gga gag cgg ccg acg ata ggg      391
Glu Ala Asn His Ala Glu Phe Pro Leu Gly Glu Arg Pro Thr Ile Gly
            25                  30                  35
ccg gag cca cca gtg aac ccc ttc cac gag tcc agc acg tgg agc atc      439
Pro Glu Pro Pro Val Asn Pro Phe His Glu Ser Ser Thr Trp Ser Ile
        40                  45                  50
ccc caa gtg atc aag acc att ctg cta gtc ccc ttg ctc gtc ata cgc      487
Pro Gln Val Ile Lys Thr Ile Leu Leu Val Pro Leu Leu Val Ile Arg
    55                  60                  65
ttg ctc agc atg ttc gct ctc atg atg ttg ggc tac ata tgc gtc aag      535
Leu Leu Ser Met Phe Ala Leu Met Met Leu Gly Tyr Ile Cys Val Lys
70                  75                  80                  85
gtc gct atg atc gga tgc aaa gac ccg ttg ttc aag cct ttc aat cct      583
Val Ala Met Ile Gly Cys Lys Asp Pro Leu Phe Lys Pro Phe Asn Pro
                90                  95                  100
ttg cgg cga ctc ttg ttg gta agt gtg agg tta ata gca aga ggg gtg      631
Leu Arg Arg Leu Leu Leu Val Ser Val Arg Leu Ile Ala Arg Gly Val
            105                 110                 115
atg gtg gcc atg ggg tat tac tat atc ctc gtc aag gga aaa cca gcc      679
Met Val Ala Met Gly Tyr Tyr Tyr Ile Leu Val Lys Gly Lys Pro Ala
        120                 125                 130
cac cgg tct gtg gcg ccc att atc gta tcc aac cac atc ggc ttt gtg      727
His Arg Ser Val Ala Pro Ile Ile Val Ser Asn His Ile Gly Phe Val
    135                 140                 145
gat ccc att ttt gtg ttc tat agg cac ttg ccg gtc atc gtc tca gcc      775
Asp Pro Ile Phe Val Phe Tyr Arg His Leu Pro Val Ile Val Ser Ala
150                 155                 160                 165
aag gaa att gtg gag atg ccc ata atc gga atg ttc tta caa gct ctg      823
```

```
          Lys Glu Ile Val Glu Met Pro Ile Ile Gly Met Phe Leu Gln Ala Leu
                      170                 175                 180
cag atc ata cct gtg gac cga ata aac ccc gcg tcc agg cac cat gcg        871
Gln Ile Ile Pro Val Asp Arg Ile Asn Pro Ala Ser Arg His His Ala
            185                 190                 195
gct gga aat atc cga cga aga gct atg gac aac gag tgg ccg cat gtc        919
Ala Gly Asn Ile Arg Arg Arg Ala Met Asp Asn Glu Trp Pro His Val
            200                 205                 210
atg ctg ttt cca gag ggg act acc aca aat ggc aaa gcg ttg atc tcc        967
Met Leu Phe Pro Glu Gly Thr Thr Thr Asn Gly Lys Ala Leu Ile Ser
        215                 220                 225
ttc aaa aca gga gca ttt tcg cct ggt cta cct gtg caa ccc atg gtc       1015
Phe Lys Thr Gly Ala Phe Ser Pro Gly Leu Pro Val Gln Pro Met Val
230                 235                 240                 245
att aaa tac ccc cac aag tat gtg aat ccg tgt tgg tgt aac caa ggg       1063
Ile Lys Tyr Pro His Lys Tyr Val Asn Pro Cys Trp Cys Asn Gln Gly
                250                 255                 260
ggg cca ttg gtc att ctc ttt cag ctg atg act cag ttt gta aat tac       1111
Gly Pro Leu Val Ile Leu Phe Gln Leu Met Thr Gln Phe Val Asn Tyr
                265                 270                 275
atg gag gtg gag tat ttg cct gtg atg acg cca aat gtg cat gag att       1159
Met Glu Val Glu Tyr Leu Pro Val Met Thr Pro Asn Val His Glu Ile
            280                 285                 290
aaa aat ccc cat gaa ttt gct aat aga gta cgg act gag atg gcc aaa       1207
Lys Asn Pro His Glu Phe Ala Asn Arg Val Arg Thr Glu Met Ala Lys
        295                 300                 305
gcg ctg ggc gtt gtg tgc acg gaa cat aac ttt cta gat atc aaa cta       1255
Ala Leu Gly Val Val Cys Thr Glu His Asn Phe Leu Asp Ile Lys Leu
310                 315                 320                 325
aaa atg gct gca gag aag ctc aag cag cct tca gga cgc tca ttg gtt       1303
Lys Met Ala Ala Glu Lys Leu Lys Gln Pro Ser Gly Arg Ser Leu Val
            330                 335                 340
gaa ttc gca cgc atg gag aag ctt ttt cga ctg gac tat tcc aag gcc       1351
Glu Phe Ala Arg Met Glu Lys Leu Phe Arg Leu Asp Tyr Ser Lys Ala
            345                 350                 355
cag gaa tac ttg gaa aaa ttc agt gct atg gat cct tca cac agt ggt       1399
Gln Glu Tyr Leu Glu Lys Phe Ser Ala Met Asp Pro Ser His Ser Gly
            360                 365                 370
tat gtc aca tac gat gag ttc ctt aaa gca ctc cat ctt ccg ccc acc       1447
Tyr Val Thr Tyr Asp Glu Phe Leu Lys Ala Leu His Leu Pro Pro Thr
        375                 380                 385
cag atc act gag cag gtg ttc aac ctt ttc gac aag aac gga cac ggt       1495
Gln Ile Thr Glu Gln Val Phe Asn Leu Phe Asp Lys Asn Gly His Gly
390                 395                 400                 405
tct ata aac ttt cga gag ttt gtg gca ggg ctt gct ttc ctg tct acc       1543
Ser Ile Asn Phe Arg Glu Phe Val Ala Gly Leu Ala Phe Leu Ser Thr
            410                 415                 420
cac act tca ttc cag act aca atg aag gct gca ttc aaa gct tgt gat       1591
His Thr Ser Phe Gln Thr Thr Met Lys Ala Ala Phe Lys Ala Cys Asp
            425                 430                 435
gtg gat ggc gat ggc acc ctc act cgt aat gag gtg gaa agc agc ttg       1639
Val Asp Gly Asp Gly Thr Leu Thr Arg Asn Glu Val Glu Ser Ser Leu
            440                 445                 450
atg gcc gta ttc ccg gag ctc ccc cca gca acg gtg tta aaa ctt ttc       1687
Met Ala Val Phe Pro Glu Leu Pro Pro Ala Thr Val Leu Lys Leu Phe
        455                 460                 465
gac acg ctg gat tta aat cgt gac ggg agc att aac tgg gag gag ttc       1735
```

```
Asp Thr Leu Asp Leu Asn Arg Asp Gly Ser Ile Asn Trp Glu Glu Phe
470                 475                 480                 485
agc agc ttt ctg caa cga aat cct gag tat ttg gcc atc ata ttg gct        1783
Ser Ser Phe Leu Gln Arg Asn Pro Glu Tyr Leu Ala Ile Ile Leu Ala
                490                 495                 500
gca cac cct act ctg ttg cag gca cca aag tcg gaa gag agt gaa act        1831
Ala His Pro Thr Leu Leu Gln Ala Pro Lys Ser Glu Glu Ser Glu Thr
            505                 510                 515
aac atc tagagttctg tcaatcgata tctattagat catctcttc acatgctgtg          1887
Asn Ile


ggacctttg gagctgcaat tcctcgagca tgatataacc actctattac agttgcgctt       1947
agtgggtgca tcttctggat ttgaatcgac tcggggacat aaaagcagca gtggtttgct       2007
gtcaccgttg acatggttta ggaacttagc atcgagatag atccttactt gagatcattt       2067
tgtatttcca cagactattg ctgttaccag tagctctgct agagctagaa tttctatgat       2127
gtggacgaaa gtcaacttat cttaagaat caaaagttaa gctccggtct ttgtaacgtt        2187
tttactgcaa aaaaaaaaaa aaaaaaaaa                                        2217


<210>  10

<211>  519

<212>  PRT
<213>  Physcomitrella patens

<400>  10

Met Thr Ser Thr Glu Asn Thr Ala Met Phe Thr Glu Asp Thr Ser Thr
1               5                   10                  15
Leu Asn Gly Ser Thr Glu Ala Asn His Ala Glu Phe Pro Leu Gly Glu
            20                  25                  30
Arg Pro Thr Ile Gly Pro Glu Pro Pro Val Asn Pro Phe His Glu Ser
            35                  40                  45
Ser Thr Trp Ser Ile Pro Gln Val Ile Lys Thr Ile Leu Leu Val Pro
        50                  55                  60
Leu Leu Val Ile Arg Leu Leu Ser Met Phe Ala Leu Met Met Leu Gly
65                  70                  75                  80
Tyr Ile Cys Val Lys Val Ala Met Ile Gly Cys Lys Asp Pro Leu Phe
                85                  90                  95
Lys Pro Phe Asn Pro Leu Arg Arg Leu Leu Leu Val Ser Val Arg Leu
            100                 105                 110
Ile Ala Arg Gly Val Met Val Ala Met Gly Tyr Tyr Tyr Ile Leu Val
            115                 120                 125
Lys Gly Lys Pro Ala His Arg Ser Val Ala Pro Ile Ile Val Ser Asn
        130                 135                 140
His Ile Gly Phe Val Asp Pro Ile Phe Val Phe Tyr Arg His Leu Pro
145                 150                 155                 160
Val Ile Val Ser Ala Lys Glu Ile Val Glu Met Pro Ile Ile Gly Met
                165                 170                 175
Phe Leu Gln Ala Leu Gln Ile Ile Pro Val Asp Arg Ile Asn Pro Ala
            180                 185                 190
Ser Arg His His Ala Ala Gly Asn Ile Arg Arg Arg Ala Met Asp Asn
            195                 200                 205
Glu Trp Pro His Val Met Leu Phe Pro Glu Gly Thr Thr Thr Asn Gly
        210                 215                 220
Lys Ala Leu Ile Ser Phe Lys Thr Gly Ala Phe Ser Pro Gly Leu Pro
225                 230                 235                 240
```

```
Val Gln Pro Met Val Ile Lys Tyr Pro His Lys Tyr Val Asn Pro Cys
            245             250                 255
Trp Cys Asn Gln Gly Gly Pro Leu Val Ile Leu Phe Gln Leu Met Thr
            260             265                 270
Gln Phe Val Asn Tyr Met Glu Val Glu Tyr Leu Pro Val Met Thr Pro
            275             280                 285
Asn Val His Glu Ile Lys Asn Pro His Glu Phe Ala Asn Arg Val Arg
        290             295             300
Thr Glu Met Ala Lys Ala Leu Gly Val Val Cys Thr Glu His Asn Phe
305             310             315                 320
Leu Asp Ile Lys Leu Lys Met Ala Ala Glu Lys Leu Lys Gln Pro Ser
            325             330                 335
Gly Arg Ser Leu Val Glu Phe Ala Arg Met Glu Lys Leu Phe Arg Leu
            340             345                 350
Asp Tyr Ser Lys Ala Gln Glu Tyr Leu Glu Lys Phe Ser Ala Met Asp
            355             360                 365
Pro Ser His Ser Gly Tyr Val Thr Tyr Asp Glu Phe Leu Lys Ala Leu
        370             375             380
His Leu Pro Pro Thr Gln Ile Thr Glu Gln Val Phe Asn Leu Phe Asp
385             390             395                 400
Lys Asn Gly His Gly Ser Ile Asn Phe Arg Glu Phe Val Ala Gly Leu
            405             410                 415
Ala Phe Leu Ser Thr His Thr Ser Phe Gln Thr Thr Met Lys Ala Ala
            420             425                 430
Phe Lys Ala Cys Asp Val Asp Gly Asp Gly Thr Leu Thr Arg Asn Glu
            435             440                 445
Val Glu Ser Ser Leu Met Ala Val Phe Pro Glu Leu Pro Pro Ala Thr
        450             455             460
Val Leu Lys Leu Phe Asp Thr Leu Asp Leu Asn Arg Asp Gly Ser Ile
465             470             475                 480
Asn Trp Glu Glu Phe Ser Ser Phe Leu Gln Arg Asn Pro Glu Tyr Leu
            485             490                 495
Ala Ile Ile Leu Ala Ala His Pro Thr Leu Leu Gln Ala Pro Lys Ser
            500             505                 510
Glu Glu Ser Glu Thr Asn Ile
            515
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<210> 11

<211> 1014

<212> DNA
<213> Physcomitrella patens

<220>
<221> CDS
<222> (1)..(1014)
<223> LPAAT

<400> 11

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atg att atg atg gag gtg ctg tgg tcg gag ctt ata tgg ctg ctg gat    48
Met Ile Met Met Glu Val Leu Trp Ser Glu Leu Ile Trp Leu Leu Asp
1               5                   10                  15
tgg tgg gca aat gtg aag gtg aag gtt tac acg cca aag gag tcg tgg    96
Trp Trp Ala Asn Val Lys Val Lys Val Tyr Thr Pro Lys Glu Ser Trp
            20              25                  30
```

```
gag cac tta gga aag gag cac gca tta ctc att tgt aat cac cgc agt    144
Glu His Leu Gly Lys Glu His Ala Leu Leu Ile Cys Asn His Arg Ser
        35                  40                  45
gac att gat tgg ctc gta gga tgg att att gcc cag aga ttg ggg tgt    192
Asp Ile Asp Trp Leu Val Gly Trp Ile Ile Ala Gln Arg Leu Gly Cys
    50                  55                  60
cta ggt ggg act cga gct gtt atg aag aag tcc acc aaa ttt ctt ccg    240
Leu Gly Gly Thr Arg Ala Val Met Lys Lys Ser Thr Lys Phe Leu Pro
65                  70                  75                  80
gtc att ggc tgg tct atg tgg ttt tca gag tat gtg ttt tta tca aga    288
Val Ile Gly Trp Ser Met Trp Phe Ser Glu Tyr Val Phe Leu Ser Arg
                85                  90                  95
gat tgg gcc aaa gat gag aag gtc ttg aag aat ggt tat tca agt ctt    336
Asp Trp Ala Lys Asp Glu Lys Val Leu Lys Asn Gly Tyr Ser Ser Leu
            100                 105                 110
aag ggc ttc ccc agg acc ttg tgg gtg gct ctt ttt gtg gaa ggc act    384
Lys Gly Phe Pro Arg Thr Leu Trp Val Ala Leu Phe Val Glu Gly Thr
        115                 120                 125
cga ttt acg aag gct aaa ctt gag gtt gcc caa aaa ttt gcg gcg gat    432
Arg Phe Thr Lys Ala Lys Leu Glu Val Ala Gln Lys Phe Ala Ala Asp
    130                 135                 140
aca ggg cta cgt gtt cca agg tat gtg ctt gtt cct cgc aca aaa ggg    480
Thr Gly Leu Arg Val Pro Arg Tyr Val Leu Val Pro Arg Thr Lys Gly
145                 150                 155                 160
ttc gtt tcg gct gtg gag aac ttg cgt gaa ttt gtt ccg gta gtt tat    528
Phe Val Ser Ala Val Glu Asn Leu Arg Glu Phe Val Pro Val Val Tyr
                165                 170                 175
gac atg acc gtt gct ata tct aaa gag ctg ccc aat cct aca atg atc    576
Asp Met Thr Val Ala Ile Ser Lys Glu Leu Pro Asn Pro Thr Met Ile
            180                 185                 190
cgg att ttc aga ggg caa cca tct gtg gtt cat gtg tac gtg agg cgg    624
Arg Ile Phe Arg Gly Gln Pro Ser Val Val His Val Tyr Val Arg Arg
        195                 200                 205
gtc cct atg tct gat ctg cct gag gga gcc aac gcg att tct aaa tgg    672
Val Pro Met Ser Asp Leu Pro Glu Gly Ala Asn Ala Ile Ser Lys Trp
    210                 215                 220
tgt cac gat gcc ttt cac atc aag gac gat cgg ctg gag cag cac gaa    720
Cys His Asp Ala Phe His Ile Lys Asp Asp Arg Leu Glu Gln His Glu
225                 230                 235                 240
aaa gag aat acg ttt ggg gag gac ttg tat att cct att gaa cgg cca    768
Lys Glu Asn Thr Phe Gly Glu Asp Leu Tyr Ile Pro Ile Glu Arg Pro
                245                 250                 255
ctt aaa cct ctt att att gtg atc tcc tgg gcc atc act ttg ctg gct    816
Leu Lys Pro Leu Ile Ile Val Ile Ser Trp Ala Ile Thr Leu Leu Ala
            260                 265                 270
gca gca tgg tgg ttt cta aga cga gtt tta tcc act tgg aaa gga atc    864
Ala Ala Trp Trp Phe Leu Arg Arg Val Leu Ser Thr Trp Lys Gly Ile
        275                 280                 285
gcc tgg gtg gca gga gta ctc gtg gtc gtc atg ctg tgt gtc cag att    912
Ala Trp Val Ala Gly Val Leu Val Val Val Met Leu Cys Val Gln Ile
        290                 295                 300
tta gtg atg tcg tca caa tcg gaa aga agt tca gat cct gca gct aag    960
Leu Val Met Ser Ser Gln Ser Glu Arg Ser Ser Asp Pro Ala Ala Lys
305                 310                 315                 320
aag gcc aat caa aaa cag gcg gct tct gtt gct cac ctc ggc aaa acg   1008
Lys Ala Asn Gln Lys Gln Ala Ala Ser Val Ala His Leu Gly Lys Thr
                325                 330                 335
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gac tga   1014
Asp

<210> 12

<211> 337
<212> PRT
<213> Physcomitrella patens

<400> 12

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Met Ile Met Met Glu Val Leu Trp Ser Glu Leu Ile Trp Leu Leu Asp
1               5                   10                  15
Trp Trp Ala Asn Val Lys Val Lys Val Tyr Thr Pro Lys Glu Ser Trp
            20                  25                  30
Glu His Leu Gly Lys Glu His Ala Leu Leu Ile Cys Asn His Arg Ser
        35                  40                  45
Asp Ile Asp Trp Leu Val Gly Trp Ile Ile Ala Gln Arg Leu Gly Cys
    50                  55                  60
Leu Gly Gly Thr Arg Ala Val Met Lys Lys Ser Thr Lys Phe Leu Pro
65                  70                  75                  80
Val Ile Gly Trp Ser Met Trp Phe Ser Glu Tyr Val Phe Leu Ser Arg
            85                  90                  95
Asp Trp Ala Lys Asp Glu Lys Val Leu Lys Asn Gly Tyr Ser Ser Leu
            100                 105                 110
Lys Gly Phe Pro Arg Thr Leu Trp Val Ala Leu Phe Val Glu Gly Thr
            115                 120                 125
Arg Phe Thr Lys Ala Lys Leu Glu Val Ala Gln Lys Phe Ala Ala Asp
    130                 135                 140
Thr Gly Leu Arg Val Pro Arg Tyr Val Leu Val Pro Arg Thr Lys Gly
145                 150                 155                 160
Phe Val Ser Ala Val Glu Asn Leu Arg Glu Phe Val Pro Val Val Tyr
            165                 170                 175
Asp Met Thr Val Ala Ile Ser Lys Glu Leu Pro Asn Pro Thr Met Ile
            180                 185                 190
Arg Ile Phe Arg Gly Gln Pro Ser Val Val His Val Tyr Val Arg Arg
            195                 200                 205
Val Pro Met Ser Asp Leu Pro Glu Gly Ala Asn Ala Ile Ser Lys Trp
    210                 215                 220
Cys His Asp Ala Phe His Ile Lys Asp Asp Arg Leu Glu Gln His Glu
225                 230                 235                 240
Lys Glu Asn Thr Phe Gly Glu Asp Leu Tyr Ile Pro Ile Glu Arg Pro
            245                 250                 255
Leu Lys Pro Leu Ile Ile Val Ile Ser Trp Ala Ile Thr Leu Leu Ala
            260                 265                 270
Ala Ala Trp Trp Phe Leu Arg Arg Val Leu Ser Thr Trp Lys Gly Ile
        275                 280                 285
Ala Trp Val Ala Gly Val Leu Val Val Val Met Leu Cys Val Gln Ile
    290                 295                 300
Leu Val Met Ser Ser Gln Ser Glu Arg Ser Ser Asp Pro Ala Ala Lys
305                 310                 315                 320
Lys Ala Asn Gln Lys Gln Ala Ala Ser Val Ala His Leu Gly Lys Thr
            325                 330                 335
Asp
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<210> 13
<211> 643

<212> DNA
<213> Physcomitrella patens

<220>
<221> misc_feature
<223> LPAAT2

<400> 13

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ggcgcgccag aggacgagac aaggggagtc aattggaatg cctgaagacc tgcatgaaac        60
tggttaaaga aggtgtgtct gctctgtttt tccctgaggg cacaaggaca acggatggag       120
caatggctgc cttcaagaaa ggagctttct ctgtggcggc caagggaggt gtgtcagttg       180
tacctataac gttaattggc tcaggcaagt tgatgccaaa tggtttagaa tatacattac       240
ggcctggcgt tgtgaaaatg attgtccacc cagctatccg cagtaaaaat gccgatgagc       300
tttgtgatca gtctaggaag gttattgcag agaccttgat caaacacggt cttcctgttc       360
attagttgct gtgattgatg atcgcctatc aggatgatgc gatcaagtga tcaagccctg       420
tttgtcgttc ttagtgatta aggagtcatt tctgtccatc gtttatgccc cgcaagagat       480
ttaaggagat cacaaagtcg gttgtagcaa gagagttgga cactgtgata agcccaatta       540
acttatgttg aagtgtcatt tattctttga aaaaaaaaa  aataaaaaaa aaaaaaaaaa       600
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaagcggc cgc                         643
```

<210> 14

<211> 657
<212> DNA
<213> Physcomitrella patens

<220>
<221> CDS
<222> (1)..(657)
<223> LPAAT

<400> 14

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atg ctg ata tta cag ccc ttc gta ctc tta ctc gac aag caa cgt aga        48
Met Leu Ile Leu Gln Pro Phe Val Leu Leu Leu Asp Lys Gln Arg Arg
1               5                   10                  15
aga gct cag cac ctt gtg aac aag gtg tgg gca att ttg aca acg tct        96
Arg Ala Gln His Leu Val Asn Lys Val Trp Ala Ile Leu Thr Thr Ser
            20                  25                  30
ttg ttt tat aaa act gag att gaa ggt tgg gaa aat ctt cca gca tct       144
Leu Phe Tyr Lys Thr Glu Ile Glu Gly Trp Glu Asn Leu Pro Ala Ser
        35                  40                  45
gat gag ggt gca gtg tat gtt gcc aat cat caa agc ttt ttg gac atc       192
Asp Glu Gly Ala Val Tyr Val Ala Asn His Gln Ser Phe Leu Asp Ile
    50                  55                  60
tat aca ctc ttt caa tta gga cga cca ttt aag ttt att agc aag acc       240
Tyr Thr Leu Phe Gln Leu Gly Arg Pro Phe Lys Phe Ile Ser Lys Thr
65                  70                  75                  80
agc aat ttt ctc att ccg att att ggt tgg tcc atg tac atg acg ggc       288
Ser Asn Phe Leu Ile Pro Ile Ile Gly Trp Ser Met Tyr Met Thr Gly
                85                  90                  95
cac att ccc cta aag cgt atg gac aag agg agt caa ttg gaa tgc ctg       336
His Ile Pro Leu Lys Arg Met Asp Lys Arg Ser Gln Leu Glu Cys Leu
```

```
                  100                        105                       110
aag acc tgc atg aag ctg gtt aaa gaa ggt gtg tct gtt ctg ttt ttc    384
Lys Thr Cys Met Lys Leu Val Lys Glu Gly Val Ser Val Leu Phe Phe
        115                     120                     125
cct gag ggc aca agg aca acg gat gga gca atg gct gcc ttc aag aaa    432
Pro Glu Gly Thr Arg Thr Thr Asp Gly Ala Met Ala Ala Phe Lys Lys
    130                     135                     140
gga gct ttc tct gtg gcg gcc aag gga ggt gtg cca gtt gta cct ata    480
Gly Ala Phe Ser Val Ala Ala Lys Gly Gly Val Pro Val Val Pro Ile
145                     150                     155                     160
acg tta att ggc tca ggc aag ttg atg cca aat ggt tta gaa tat aca    528
Thr Leu Ile Gly Ser Gly Lys Leu Met Pro Asn Gly Leu Glu Tyr Thr
                165                     170                     175
tta cgg cct ggc gtt gtg aaa atg att gtc cac cca gct atc cgc agt    576
Leu Arg Pro Gly Val Val Lys Met Ile Val His Pro Ala Ile Arg Ser
            180                     185                     190
aaa aat gcc gat gag ctt tgt gat cag tct agg aag gtt att gca gag    624
Lys Asn Ala Asp Glu Leu Cys Asp Gln Ser Arg Lys Val Ile Ala Glu
        195                     200                     205
acc ttg atc caa cac ggt ctt cct gtt cat tag                        657
Thr Leu Ile Gln His Gly Leu Pro Val His
    210                     215
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<210> 15

<211> 218
<212> PRT
<213> Physcomitrella patens

<400> 15

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Met Leu Ile Leu Gln Pro Phe Val Leu Leu Leu Asp Lys Gln Arg Arg
1                   5                   10                  15
Arg Ala Gln His Leu Val Asn Lys Val Trp Ala Ile Leu Thr Thr Ser
            20                  25                  30
Leu Phe Tyr Lys Thr Glu Ile Glu Gly Trp Glu Asn Leu Pro Ala Ser
        35                  40                  45
Asp Glu Gly Ala Val Tyr Val Ala Asn His Gln Ser Phe Leu Asp Ile
    50                  55                  60
Tyr Thr Leu Phe Gln Leu Gly Arg Pro Phe Lys Phe Ile Ser Lys Thr
65                  70                  75                  80
Ser Asn Phe Leu Ile Pro Ile Ile Gly Trp Ser Met Tyr Met Thr Gly
                85                  90                  95
His Ile Pro Leu Lys Arg Met Asp Lys Arg Ser Gln Leu Glu Cys Leu
            100                 105                 110
Lys Thr Cys Met Lys Leu Val Lys Glu Gly Val Ser Val Leu Phe Phe
        115                 120                 125
Pro Glu Gly Thr Arg Thr Thr Asp Gly Ala Met Ala Ala Phe Lys Lys
    130                 135                 140
Gly Ala Phe Ser Val Ala Ala Lys Gly Gly Val Pro Val Val Pro Ile
145                 150                 155                 160
Thr Leu Ile Gly Ser Gly Lys Leu Met Pro Asn Gly Leu Glu Tyr Thr
                165                 170                 175
Leu Arg Pro Gly Val Val Lys Met Ile Val His Pro Ala Ile Arg Ser
            180                 185                 190
Lys Asn Ala Asp Glu Leu Cys Asp Gln Ser Arg Lys Val Ile Ala Glu
        195                 200                 205
```

```
Thr Leu Ile Gln His Gly Leu Pro Val His
    210                 215
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<210> 16

<211> 1254
<212> DNA
<213> Mortierella alpina

<220>
<221> CDS
<222> (1)..(1251)
<223> LPAAT

<400> 16

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atg gat gaa tcc acc acg acc acc acg cac cac tca gag acc agc agc    48
Met Asp Glu Ser Thr Thr Thr Thr Thr His His Ser Glu Thr Ser Ser
1               5                   10                  15
aag acg tcc tcg cac ccc cgc cgg ctc ggt ccc gag atg aac cct atc    96
Lys Thr Ser Ser His Pro Arg Arg Leu Gly Pro Glu Met Asn Pro Ile
                20                  25                  30
tac aag ggt ctg cga gcc att gtc tgg gcc ttt tac ttc aac ctg gga   144
Tyr Lys Gly Leu Arg Ala Ile Val Trp Ala Phe Tyr Phe Asn Leu Gly
            35                  40                  45
gcg tcg ctt ata tcg atc acg cag gtg ctg tcg ctg cct ctg gcg ttg   192
Ala Ser Leu Ile Ser Ile Thr Gln Val Leu Ser Leu Pro Leu Ala Leu
        50                  55                  60
att gct cca ggg gtc tac cag tgg cac atc agc aaa aca cag ggt cac   240
Ile Ala Pro Gly Val Tyr Gln Trp His Ile Ser Lys Thr Gln Gly His
65                  70                  75                  80
ttt gga gct ttc ctg ctc cgg atg aac cag ctc ttt gcg ccg tca gat   288
Phe Gly Ala Phe Leu Leu Arg Met Asn Gln Leu Phe Ala Pro Ser Asp
                85                  90                  95
att gtc ttg aca ggg gac gag agt gtc agg gga atc gtc aag gtc tac   336
Ile Val Leu Thr Gly Asp Glu Ser Val Arg Gly Ile Val Lys Val Tyr
            100                 105                 110
aaa gga cgg aac ctg aag gag gcc ggt gag cca ggc agc ggt cag gga   384
Lys Gly Arg Asn Leu Lys Glu Ala Gly Glu Pro Gly Ser Gly Gln Gly
        115                 120                 125
gag gac att ctt ctg gat atg ccc gag agg atg gtt ttc att gcg aac   432
Glu Asp Ile Leu Leu Asp Met Pro Glu Arg Met Val Phe Ile Ala Asn
    130                 135                 140
cac cag atc tac tct gac tgg atg tac ctc tgg tgc ttc tcc tat ttt   480
His Gln Ile Tyr Ser Asp Trp Met Tyr Leu Trp Cys Phe Ser Tyr Phe
145                 150                 155                 160
gca gag agg cac agg gca ctg aag att att ctt cgg ggc gac ctg acc   528
Ala Glu Arg His Arg Ala Leu Lys Ile Ile Leu Arg Gly Asp Leu Thr
                165                 170                 175
tgg atc cct gtc ttt ggc tgg ggt atg cgg ttc ttt gac ttt atc ttt   576
Trp Ile Pro Val Phe Gly Trp Gly Met Arg Phe Phe Asp Phe Ile Phe
            180                 185                 190
ttg aaa cgt aat gac tgg gca cac gat cgc cgt gcc att gag gaa aac   624
Leu Lys Arg Asn Asp Trp Ala His Asp Arg Arg Ala Ile Glu Glu Asn
        195                 200                 205
ttg gga cgt gtc aag gaa aag gat ccc ctc tgg ctc gtg gtc ttc ccc   672
Leu Gly Arg Val Lys Glu Lys Asp Pro Leu Trp Leu Val Val Phe Pro
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        210                      215                      220
gag gga aca gtc gtc tcc aag gaa acg cgt ctc cga tcc gtt gcc ttt      720
Glu Gly Thr Val Val Ser Lys Glu Thr Arg Leu Arg Ser Val Ala Phe
225                      230                      235                      240
tca aag aag gct agt ctg tcg gat cac cgc cat gtg ctg ctt cca agg      768
Ser Lys Lys Ala Ser Leu Ser Asp His Arg His Val Leu Leu Pro Arg          .
                        245                      250                      255
acc agc ggt ctg ttt gtg tgc atc aac aag ttg cgt gga tct gtc gac      816
Thr Ser Gly Leu Phe Val Cys Ile Asn Lys Leu Arg Gly Ser Val Asp
                260                      265                      270
tac ttg tac gat gca acc gtt ggc tac tcg aat gtc gag tat ggc gag      864
Tyr Leu Tyr Asp Ala Thr Val Gly Tyr Ser Asn Val Glu Tyr Gly Glu
            275                      280                      285
att ccg cag gag ctt tac ccg tta cca gga ctg tat atc aac aaa gca      912
Ile Pro Gln Glu Leu Tyr Pro Leu Pro Gly Leu Tyr Ile Asn Lys Ala
        290                      295                      300
cag ccc aag gag atc aac atg cac ctg cgt cga ttt gcg atc aag gat      960
Gln Pro Lys Glu Ile Asn Met His Leu Arg Arg Phe Ala Ile Lys Asp
305                      310                      315                      320
atc ccc acg tca gaa ccc gaa ttt gtg gaa tgg gtc cga gct cgg tgg     1008
Ile Pro Thr Ser Glu Pro Glu Phe Val Glu Trp Val Arg Ala Arg Trp  .
                        325                      330                      335
gtg gag aag gat gag ttg atg gaa gag ttt tat acc aag ggc cga ttt     1056
Val Glu Lys Asp Glu Leu Met Glu Glu Phe Tyr Thr Lys Gly Arg Phe
                340                      345                      350
cca tca caa ctg acg gcc gcc gac att ggt gag aag gag gtc aag acg     1104
Pro Ser Gln Leu Thr Ala Ala Asp Ile Gly Glu Lys Glu Val Lys Thr
            355                      360                      365
gca gga ggt cca acg gag gga cag agt gtc agg atc ccg ctc aag gcg     1152
Ala Gly Gly Pro Thr Glu Gly Gln Ser Val Arg Ile Pro Leu Lys Ala
        370                      375                      380
cga ggc atg atg gac tac ctc atg ccc tcg gtc atg aat ctg atc gcc     1200
Arg Gly Met Met Asp Tyr Leu Met Pro Ser Val Met Asn Leu Ile Ala
385                      390                      395                      400
ctt cct gtg ctg gcg ttt gcg atg aga tat gca gtg cag caa gca tcg     1248
Leu Pro Val Leu Ala Phe Ala Met Arg Tyr Ala Val Gln Gln Ala Ser
            405                      410                      415
ggc tga                                                              1254
Gly


<210>  17

<211>  417
<212>  PRT
<213>  Mortierella alpina

<400>  17

Met Asp Glu Ser Thr Thr Thr Thr Thr His His Ser Glu Thr Ser Ser
1               5                       10                      15
Lys Thr Ser Ser His Pro Arg Arg Leu Gly Pro Glu Met Asn Pro Ile
            20                      25                      30
Tyr Lys Gly Leu Arg Ala Ile Val Trp Ala Phe Tyr Phe Asn Leu Gly
        35                      40                      45
Ala Ser Leu Ile Ser Ile Thr Gln Val Leu Ser Leu Pro Leu Ala Leu
        50                      55                      60
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Ile Ala Pro Gly Val Tyr Gln Trp His Ile Ser Lys Thr Gln Gly His
65   70   75   80
Phe Gly Ala Phe Leu Leu Arg Met Asn Gln Leu Phe Ala Pro Ser Asp
                85   90   95
Ile Val Leu Thr Gly Asp Glu Ser Val Arg Gly Ile Val Lys Val Tyr
            100   105   110
Lys Gly Arg Asn Leu Lys Glu Ala Gly Glu Pro Gly Ser Gly Gln Gly
            115   120   125
Glu Asp Ile Leu Leu Asp Met Pro Glu Arg Met Val Phe Ile Ala Asn
    130   135   140
His Gln Ile Tyr Ser Asp Trp Met Tyr Leu Trp Cys Phe Ser Tyr Phe
145   150   155   160
Ala Glu Arg His Arg Ala Leu Lys Ile Ile Leu Arg Gly Asp Leu Thr
            165   170   175
Trp Ile Pro Val Phe Gly Trp Gly Met Arg Phe Phe Asp Phe Ile Phe
            180   185   190
Leu Lys Arg Asn Asp Trp Ala His Asp Arg Arg Ala Ile Glu Glu Asn
            195   200   205
Leu Gly Arg Val Lys Glu Lys Asp Pro Leu Trp Leu Val Val Phe Pro
    210   215   220
Glu Gly Thr Val Val Ser Lys Glu Thr Arg Leu Arg Ser Val Ala Phe
225   230   235   240
Ser Lys Lys Ala Ser Leu Ser Asp His Arg His Val Leu Leu Pro Arg
            245   250   255
Thr Ser Gly Leu Phe Val Cys Ile Asn Lys Leu Arg Gly Ser Val Asp
            260   265   270
Tyr Leu Tyr Asp Ala Thr Val Gly Tyr Ser Asn Val Glu Tyr Gly Glu
            275   280   285
Ile Pro Gln Glu Leu Tyr Pro Leu Pro Gly Leu Tyr Ile Asn Lys Ala
    290   295   300
Gln Pro Lys Glu Ile Asn Met His Leu Arg Arg Phe Ala Ile Lys Asp
305   310   315   320
Ile Pro Thr Ser Glu Pro Glu Phe Val Glu Trp Val Arg Ala Arg Trp
            325   330   335
Val Glu Lys Asp Glu Leu Met Glu Glu Phe Tyr Thr Lys Gly Arg Phe
            340   345   350
Pro Ser Gln Leu Thr Ala Ala Asp Ile Gly Glu Lys Glu Val Lys Thr
    355   360   365
Ala Gly Gly Pro Thr Glu Gly Gln Ser Val Arg Ile Pro Leu Lys Ala
    370   375   380
Arg Gly Met Met Asp Tyr Leu Met Pro Ser Val Met Asn Leu Ile Ala
385   390   395   400
Leu Pro Val Leu Ala Phe Ala Met Arg Tyr Ala Val Gln Gln Ala Ser
            405   410   415
Gly

<210> 18

<211> 1170
<212> DNA
<213> Mortierella alpina

<220>
<221> CDS
<222> (1)..(1167)
<223> LPAAT

<400> 18

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1               5                   10                  15
ttc aac ctg gga gcg tcg ctt ata tcg atc acg cag gtg ctg tcg ctg        96
Phe Asn Leu Gly Ala Ser Leu Ile Ser Ile Thr Gln Val Leu Ser Leu
                20                  25                  30
cct ctg gcg ttg att gct cca ggg gtc tac cag tgg cac atc agc aaa       144
Pro Leu Ala Leu Ile Ala Pro Gly Val Tyr Gln Trp His Ile Ser Lys
            35                  40                  45
aca cag ggt cac ttt gga gct ttc ctg ctc cgg atg aac cag ctc ttt       192
Thr Gln Gly His Phe Gly Ala Phe Leu Leu Arg Met Asn Gln Leu Phe
        50                  55                  60
gcg ccg tca gat att gtc ttg aca ggg gac gag agt gtc agg gga atc       240
Ala Pro Ser Asp Ile Val Leu Thr Gly Asp Glu Ser Val Arg Gly Ile
65                  70                  75                  80
gtc aag gtc tac aaa gga cgg aac ctg aag gag gcc ggt gag cca ggc       288
Val Lys Val Tyr Lys Gly Arg Asn Leu Lys Glu Ala Gly Glu Pro Gly
                85                  90                  95
agc ggt cag gga gag gac att ctt ctg gat atg ccc gag agg atg gtt       336
Ser Gly Gln Gly Glu Asp Ile Leu Leu Asp Met Pro Glu Arg Met Val
            100                 105                 110
ttc att gcg aac cac cag atc tac tct gac tgg atg tac ctc tgg tgc       384
Phe Ile Ala Asn His Gln Ile Tyr Ser Asp Trp Met Tyr Leu Trp Cys
        115                 120                 125
ttc tcc tat ttt gca gag agg cac agg gca ctg aag att att ctt cgg       432
Phe Ser Tyr Phe Ala Glu Arg His Arg Ala Leu Lys Ile Ile Leu Arg
        130                 135                 140
ggc gac ctg acc tgg atc cct gtc ttt ggc tgg ggt atg cgg ttc ttt       480
Gly Asp Leu Thr Trp Ile Pro Val Phe Gly Trp Gly Met Arg Phe Phe
145                 150                 155                 160
gac ttt atc ttt ttg aaa cgt aat gac tgg gca cac gat cgc cgt gcc       528
Asp Phe Ile Phe Leu Lys Arg Asn Asp Trp Ala His Asp Arg Arg Ala
                165                 170                 175
att gag gaa aac ttg gga cgt gtc aag gaa aag gat ccc ctc tgg ctc       576
Ile Glu Glu Asn Leu Gly Arg Val Lys Glu Lys Asp Pro Leu Trp Leu
            180                 185                 190
gtg gtc ttc ccc gag gga aca gtc gtc tcc aag gaa acg cgt ctc cga       624
Val Val Phe Pro Glu Gly Thr Val Val Ser Lys Glu Thr Arg Leu Arg
            195                 200                 205
tcc gtt gcc ttt tca aag aag gct agt ctg tcg gat cac cgc cat gtg       672
Ser Val Ala Phe Ser Lys Lys Ala Ser Leu Ser Asp His Arg His Val
            210                 215                 220
ctg ctt cca agg acc agc ggt ctg ttt gtg tgc atc aac aag ttg cgt       720
Leu Leu Pro Arg Thr Ser Gly Leu Phe Val Cys Ile Asn Lys Leu Arg
225                 230                 235                 240
gga tct gtc gac tac ttg tac gat gca acc gtt ggc tac tcg aat gtc       768
Gly Ser Val Asp Tyr Leu Tyr Asp Ala Thr Val Gly Tyr Ser Asn Val
                245                 250                 255
gag tat ggc gag att ccg cag gag ctt tac ccg tta cca gga ctg tat       816
Glu Tyr Gly Glu Ile Pro Gln Glu Leu Tyr Pro Leu Pro Gly Leu Tyr
            260                 265                 270
atc aac aaa gca cag ccc aag gag atc aac atg cac ctg cgt cga ttt       864
Ile Asn Lys Ala Gln Pro Lys Glu Ile Asn Met His Leu Arg Arg Phe
        275                 280                 285
gcg atc aag gat atc ccc acg tca gaa ccc gaa ttt gtg gaa tgg gtc       912
Ala Ile Lys Asp Ile Pro Thr Ser Glu Pro Glu Phe Val Glu Trp Val
```

```
Ala Ile Lys Asp Ile Pro Thr Ser Glu Pro Glu Phe Val Glu Trp Val
    290                 295                 300
cga gct cgg tgg gtg gag aag gat gag ttg atg gaa gag ttt tat acc      960
Arg Ala Arg Trp Val Glu Lys Asp Glu Leu Met Glu Glu Phe Tyr Thr
305                 310                 315                 320
aag ggc cga ttt cca tca caa ctg acg gcc gcc gac att ggt gag aag     1008
Lys Gly Arg Phe Pro Ser Gln Leu Thr Ala Ala Asp Ile Gly Glu Lys
                325                 330                 335
gag gtc aag acg gca gga ggt cca acg gag gga cag agt gtc agg atc     1056
Glu Val Lys Thr Ala Gly Gly Pro Thr Glu Gly Gln Ser Val Arg Ile
                340                 345                 350
ccg ctc aag gcg cga ggc atg atg gac tac ctc atg ccc tcg gtc atg     1104
Pro Leu Lys Ala Arg Gly Met Met Asp Tyr Leu Met Pro Ser Val Met
            355                 360                 365
aat ctg atc gcc ctt cct gtg ctg gcg ttt gcg atg aga tat gca gtg     1152
Asn Leu Ile Ala Leu Pro Val Leu Ala Phe Ala Met Arg Tyr Ala Val
    370                 375                 380
cag caa gca tcg ggc tga                                             1170
Gln Gln Ala Ser Gly
385
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<210> 19

<211> 389
<212> PRT
<213> Mortierella alpina

<400> 19

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Met Asn Pro Ile Tyr Lys Gly Leu Arg Ala Ile Val Trp Ala Phe Tyr
1               5               10              15
Phe Asn Leu Gly Ala Ser Leu Ile Ser Ile Thr Gln Val Leu Ser Leu
            20              25              30
Pro Leu Ala Leu Ile Ala Pro Gly Val Tyr Gln Trp His Ile Ser Lys
        35              40              45
Thr Gln Gly His Phe Gly Ala Phe Leu Leu Arg Met Asn Gln Leu Phe
    50              55              60
Ala Pro Ser Asp Ile Val Leu Thr Gly Asp Glu Ser Val Arg Gly Ile
65              70              75              80
Val Lys Val Tyr Lys Gly Arg Asn Leu Lys Glu Ala Gly Glu Pro Gly
            85              90              95
Ser Gly Gln Gly Glu Asp Ile Leu Leu Asp Met Pro Glu Arg Met Val
            100             105             110
Phe Ile Ala Asn His Gln Ile Tyr Ser Asp Trp Met Tyr Leu Trp Cys
            115             120             125
Phe Ser Tyr Phe Ala Glu Arg His Arg Ala Leu Lys Ile Ile Leu Arg
        130             135             140
Gly Asp Leu Thr Trp Ile Pro Val Phe Gly Trp Gly Met Arg Phe Phe
145             150             155             160
Asp Phe Ile Phe Leu Lys Arg Asn Asp Trp Ala His Asp Arg Arg Ala
            165             170             175
Ile Glu Glu Asn Leu Gly Arg Val Lys Glu Lys Asp Pro Leu Trp Leu
        180             185             190
Val Val Phe Pro Glu Gly Thr Val Val Ser Lys Glu Thr Arg Leu Arg
        195             200             205
Ser Val Ala Phe Ser Lys Lys Ala Ser Leu Ser Asp His Arg His Val
    210             215             220
```

```
Leu Leu Pro Arg Thr Ser Gly Leu Phe Val Cys Ile Asn Lys Leu Arg
225             230             235                 240
Gly Ser Val Asp Tyr Leu Tyr Asp Ala Thr Val Gly Tyr Ser Asn Val
            245             250                 255
Glu Tyr Gly Glu Ile Pro Gln Glu Leu Tyr Pro Leu Pro Gly Leu Tyr
        260             265                 270
Ile Asn Lys Ala Gln Pro Lys Glu Ile Asn Met His Leu Arg Arg Phe
        275             280                 285
Ala Ile Lys Asp Ile Pro Thr Ser Glu Pro Glu Phe Val Glu Trp Val
        290             295                 300
Arg Ala Arg Trp Val Glu Lys Asp Glu Leu Met Glu Glu Phe Tyr Thr
305             310             315                 320
Lys Gly Arg Phe Pro Ser Gln Leu Thr Ala Ala Asp Ile Gly Glu Lys
                325             330                 335
Glu Val Lys Thr Ala Gly Gly Pro Thr Glu Gly Gln Ser Val Arg Ile
            340             345                 350
Pro Leu Lys Ala Arg Gly Met Met Asp Tyr Leu Met Pro Ser Val Met
            355             360                 365
Asn Leu Ile Ala Leu Pro Val Leu Ala Phe Ala Met Arg Tyr Ala Val
            370             375                 380
Gln Gln Ala Ser Gly
385


<210>  20

<211>  687
<212>  DNA
<213>  Shewanella hanedai

<220>
<221>  CDS
<222>  (1)..(684)
<223>  LPAAT

<400>  20


atg tta ctg cta gca ttt gtt ttt ggt ggt ctt gtt tgt tta tta aga      48
Met Leu Leu Leu Ala Phe Val Phe Gly Gly Leu Val Cys Leu Leu Arg
1               5                   10                  15
ccg aga cat cgt gac aat gta cac atg ttc gct aaa att ttc tcc tat      96
Pro Arg His Arg Asp Asn Val His Met Phe Ala Lys Ile Phe Ser Tyr
                20                  25                  30
gct gcg cca gta tta ggt atc aag gtc ata gta cgt aaa cct agc gta     144
Ala Ala Pro Val Leu Gly Ile Lys Val Ile Val Arg Lys Pro Ser Val
            35                  40                  45
gcg acg act gag cct tgt gtc ttt ttg gca aat cat cag aat aat ttc     192
Ala Thr Thr Glu Pro Cys Val Phe Leu Ala Asn His Gln Asn Asn Phe
        50                  55                  60
gat atg ttt acc cat act gcg gca gta ccg aaa ggg acg gtc agt ctt     240
Asp Met Phe Thr His Thr Ala Ala Val Pro Lys Gly Thr Val Ser Leu
65                  70                  75                  80
gga aag aag agt tta gct tgg gtg cct ttt ttt ggt cag att tac tgg     288
Gly Lys Lys Ser Leu Ala Trp Val Pro Phe Phe Gly Gln Ile Tyr Trp
                85                  90                  95
ttg tcc ggt aat att cta att gac aga aaa aac cgc aat aga gcg ttt     336
Leu Ser Gly Asn Ile Leu Ile Asp Arg Lys Asn Arg Asn Arg Ala Phe
                100                 105                 110
```

```
gaa acc atg gcg caa acc gcc aaa aag att aaa gat aag tgc tta tct      384
Glu Thr Met Ala Gln Thr Ala Lys Lys Ile Lys Asp Lys Cys Leu Ser
        115                 120                 125
atc tgg ata ttt ccg gaa ggt acg cgc tct cgt ggc aag ggc tta ttg      432
Ile Trp Ile Phe Pro Glu Gly Thr Arg Ser Arg Gly Lys Gly Leu Leu
    130                 135                 140
cct ttt aaa tct ggt gca ttt cat act gca ata gat gcg gga gtg gct      480
Pro Phe Lys Ser Gly Ala Phe His Thr Ala Ile Asp Ala Gly Val Ala
145                 150                 155                 160
atg gta cct gtg ttg gca tca aat caa agc cat ata aaa ctt aat cgt      528
Met Val Pro Val Leu Ala Ser Asn Gln Ser His Ile Lys Leu Asn Arg
                165                 170                 175
tgg aat aat ggt gtg gtt att atc gag atg atg gat cca atc gaa act      576
Trp Asn Asn Gly Val Val Ile Ile Glu Met Met Asp Pro Ile Glu Thr
                180                 185                 190
aaa ggt ttg gct aag tct cag gta aag gag ttg tct aaa cgt atc cac      624
Lys Gly Leu Ala Lys Ser Gln Val Lys Glu Leu Ser Lys Arg Ile His
            195                 200                 205
gct atg atg tcg aat cgt tta act cag ttg gat caa gaa gct tca gcc      672
Ala Met Met Ser Asn Arg Leu Thr Gln Leu Asp Gln Glu Ala Ser Ala
        210                 215                 220
tta atg gca aag taa                                                   687
Leu Met Ala Lys
225
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<210> 21

<211> 228
<212> PRT
<213> Shewanella hanedai

<400> 21

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Met Leu Leu Leu Ala Phe Val Phe Gly Gly Leu Val Cys Leu Leu Arg
1               5                   10                  15
Pro Arg His Arg Asp Asn Val His Met Phe Ala Lys Ile Phe Ser Tyr
            20                  25                  30
Ala Ala Pro Val Leu Gly Ile Lys Val Ile Val Arg Lys Pro Ser Val
        35                  40                  45
Ala Thr Thr Glu Pro Cys Val Phe Leu Ala Asn His Gln Asn Asn Phe
    50                  55                  60
Asp Met Phe Thr His Thr Ala Ala Val Pro Lys Gly Thr Val Ser Leu
65                  70                  75                  80
Gly Lys Lys Ser Leu Ala Trp Val Pro Phe Phe Gly Gln Ile Tyr Trp
            85                  90                  95
Leu Ser Gly Asn Ile Leu Ile Asp Arg Lys Asn Arg Asn Arg Ala Phe
            100                 105                 110
Glu Thr Met Ala Gln Thr Ala Lys Lys Ile Lys Asp Lys Cys Leu Ser
        115                 120                 125
Ile Trp Ile Phe Pro Glu Gly Thr Arg Ser Arg Gly Lys Gly Leu Leu
    130                 135                 140
Pro Phe Lys Ser Gly Ala Phe His Thr Ala Ile Asp Ala Gly Val Ala
145                 150                 155                 160
Met Val Pro Val Leu Ala Ser Asn Gln Ser His Ile Lys Leu Asn Arg
                165                 170                 175
Trp Asn Asn Gly Val Val Ile Ile Glu Met Met Asp Pro Ile Glu Thr
                180                 185                 190
```

```
Lys Gly Leu Ala Lys Ser Gln Val Lys Glu Leu Ser Lys Arg Ile His
        195                 200                 205
Ala Met Met Ser Asn Arg Leu Thr Gln Leu Asp Gln Glu Ala Ser Ala
        210                 215                 220
Leu Met Ala Lys
225
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<210> 22

<211> 1352
<212> DNA
<213> Physcomitrella patens

<220>
<221> CDS
<222> (39)..(1340)
<223> GPAT

<400> 22

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                                             Met Pro Ser Leu Phe Arg
                                              1               5
gcg aaa cgc aat ggc aga agg acg ccg ggg aat gcc gtg acc aat ttc      104
Ala Lys Arg Asn Gly Arg Arg Thr Pro Gly Asn Ala Val Thr Asn Phe
            10                  15                  20
ggg aaa tct gaa ttc cat cgt gaa att agt ggg agt acg cgg gcg acc      152
Gly Lys Ser Glu Phe His Arg Glu Ile Ser Gly Ser Thr Arg Ala Thr
            25                  30                  35
acg cag gtg gct gaa gcc acc aca gct ggt ctt agg gag acc att gag      200
Thr Gln Val Ala Glu Ala Thr Thr Ala Gly Leu Arg Glu Thr Ile Glu
        40                  45                  50
gac cgc gct att atc gac ggt cat tct cac agt ttt gaa gga att caa      248
Asp Arg Ala Ile Ile Asp Gly His Ser His Ser Phe Glu Gly Ile Gln
55                  60                  65                  70
tcg gaa gaa gag ttg atg cag gta att gaa aag gag gtg gaa tcc ggt      296
Ser Glu Glu Glu Leu Met Gln Val Ile Glu Lys Glu Val Glu Ser Gly
            75                  80                  85
cgg ctg ccg aag cgt gct ggc gcg gga atg gta gag ttg tat cgc aat      344
Arg Leu Pro Lys Arg Ala Gly Ala Gly Met Val Glu Leu Tyr Arg Asn
            90                  95                  100
tat cga gat gct gta gtg agc agt ggc gta gaa aat gcg atg gat att      392
Tyr Arg Asp Ala Val Val Ser Ser Gly Val Glu Asn Ala Met Asp Ile
        105                 110                 115
gtt gtg aaa gtc atg tca act gtg ttg gac cgg att ctt ctg cag ttc      440
Val Val Lys Val Met Ser Thr Val Leu Asp Arg Ile Leu Leu Gln Phe
        120                 125                 130
gag gag cca ttc aca ttt gga tcg cac cac aag aga atg gtg gag ccg      488
Glu Glu Pro Phe Thr Phe Gly Ser His His Lys Arg Met Val Glu Pro
135                 140                 145                 150
tat gat tac tac aca ttt ggt cag aac tat gtg cgt cct ctc cta gat      536
Tyr Asp Tyr Tyr Thr Phe Gly Gln Asn Tyr Val Arg Pro Leu Leu Asp
                155                 160                 165
ttc agg aac tct tac ctt ggg aac tta aag atc ttt gac cag ata gag      584
Phe Arg Asn Ser Tyr Leu Gly Asn Leu Lys Ile Phe Asp Gln Ile Glu
            170                 175                 180
aag aac ctg aaa gag ggg cac aac gtc att ttt cta tcc aat cac cag      632
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```
Lys Asn Leu Lys Glu Gly His Asn Val Ile Phe Leu Ser Asn His Gln
        185                 190                 195
act gag gca gat cct gct gtt atg gcg ctg ttg ctt gag cac tct cac    680
Thr Glu Ala Asp Pro Ala Val Met Ala Leu Leu Leu Glu His Ser His
        200                 205                 210
ccc tat ttg gca gag aac ttg acc tat gtg gct gga gac agg gtt gtg    728
Pro Tyr Leu Ala Glu Asn Leu Thr Tyr Val Ala Gly Asp Arg Val Val
215                 220                 225                 230
ctg gat cca ttc tgc aaa cct ttt agt atg ggc agg aat ctc ttg tgc    776
Leu Asp Pro Phe Cys Lys Pro Phe Ser Met Gly Arg Asn Leu Leu Cys
                235                 240                 245
gtg tat tca aaa aag cac att cac gat gta ccg gac ctt gct gaa atg    824
Val Tyr Ser Lys Lys His Ile His Asp Val Pro Asp Leu Ala Glu Met
                250                 255                 260
aaa atc aaa gct aat gcg aag act ttg aga cag atg acg atc ctg ctg    872
Lys Ile Lys Ala Asn Ala Lys Thr Leu Arg Gln Met Thr Ile Leu Leu
                265                 270                 275
agg cag gga ggt caa tta tta tgg gta gca ccc agt ggt gga cgc gat    920
Arg Gln Gly Gly Gln Leu Leu Trp Val Ala Pro Ser Gly Gly Arg Asp
        280                 285                 290
cgc cct gat cct gag acc aac gaa tgg gtt cct gca cat ttt gac tcg    968
Arg Pro Asp Pro Glu Thr Asn Glu Trp Val Pro Ala His Phe Asp Ser
295                 300                 305                 310
tct gct gtg gag aat atg aag cga cta tct gac att gtc cga gta cct    1016
Ser Ala Val Glu Asn Met Lys Arg Leu Ser Asp Ile Val Arg Val Pro
                315                 320                 325
gct cat tta cat gcc cta tca tta cta tgt ttt gag att atg cca cct    1064
Ala His Leu His Ala Leu Ser Leu Leu Cys Phe Glu Ile Met Pro Pro
                330                 335                 340
cct gtc cag gta caa aag gag cta gga gag cga aga gca gta gga ttt    1112
Pro Val Gln Val Gln Lys Glu Leu Gly Glu Arg Arg Ala Val Gly Phe
                345                 350                 355
agc gga gtt ggt cta gcc gtt tcc gag caa cta gat tat gat tcc att    1160
Ser Gly Val Gly Leu Ala Val Ser Glu Gln Leu Asp Tyr Asp Ser Ile
        360                 365                 370
gcg aag tta gtc gac gat tcc aaa aat gcg aag gat gcc ttt tcg gat    1208
Ala Lys Leu Val Asp Asp Ser Lys Asn Ala Lys Asp Ala Phe Ser Asp
375                 380                 385                 390
gcg gca tgg agc gaa gtc aat gat atg tat aac gtg tta aaa gaa gca    1256
Ala Ala Trp Ser Glu Val Asn Asp Met Tyr Asn Val Leu Lys Glu Ala
                395                 400                 405
att tat ggt gac caa ggt tgt gct gtt agc aca gat tcc ttg aga ctg    1304
Ile Tyr Gly Asp Gln Gly Cys Ala Val Ser Thr Asp Ser Leu Arg Leu
        410                 415                 420
gaa cag ccc tgg ttt gat gga agc agg cga act gat tgaaaatagg gc     1352
Glu Gln Pro Trp Phe Asp Gly Ser Arg Arg Thr Asp
        425                 430
```

<210> 23

<211> 434
<212> PRT
<213> Physcomitrella patens

<400> 23

```
Met Pro Ser Leu Phe Arg Ala Lys Arg Asn Gly Arg Arg Thr Pro Gly
```

```
1                    5                         10                        15
Asn Ala Val Thr Asn Phe Gly Lys Ser Glu Phe His Arg Glu Ile Ser
                20                        25                        30
Gly Ser Thr Arg Ala Thr Thr Gln Val Ala Glu Ala Thr Thr Ala Gly
            35                        40                        45
Leu Arg Glu Thr Ile Glu Asp Arg Ala Ile Ile Asp Gly His Ser His
        50                        55                        60
Ser Phe Glu Gly Ile Gln Ser Glu Glu Glu Leu Met Gln Val Ile Glu
65                        70                        75                    80
Lys Glu Val Glu Ser Gly Arg Leu Pro Lys Arg Ala Gly Ala Gly Met
                85                        90                        95
Val Glu Leu Tyr Arg Asn Tyr Arg Asp Ala Val Val Ser Ser Gly Val
                100                       105                       110
Glu Asn Ala Met Asp Ile Val Val Lys Val Met Ser Thr Val Leu Asp
            115                       120                       125
Arg Ile Leu Leu Gln Phe Glu Glu Pro Phe Thr Phe Gly Ser His His
        130                       135                       140
Lys Arg Met Val Glu Pro Tyr Asp Tyr Tyr Thr Phe Gly Gln Asn Tyr
145                       150                       155                   160
Val Arg Pro Leu Leu Asp Phe Arg Asn Ser Tyr Leu Gly Asn Leu Lys
                165                       170                       175
Ile Phe Asp Gln Ile Glu Lys Asn Leu Lys Glu Gly His Asn Val Ile
                180                       185                       190
Phe Leu Ser Asn His Gln Thr Glu Ala Asp Pro Ala Val Met Ala Leu
                195                       200                       205
Leu Leu Glu His Ser His Pro Tyr Leu Ala Glu Asn Leu Thr Tyr Val
        210                       215                       220
Ala Gly Asp Arg Val Val Leu Asp Pro Phe Cys Lys Pro Phe Ser Met
225                       230                       235                   240
Gly Arg Asn Leu Leu Cys Val Tyr Ser Lys Lys His Ile His Asp Val
                245                       250                       255
Pro Asp Leu·Ala Glu Met Lys Ile Lys Ala Asn Ala Lys Thr Leu Arg
            260                       265                       270
Gln Met Thr Ile Leu Leu Arg Gln Gly Gly Gln Leu Leu Trp Val Ala
        275                       280                       285
Pro Ser Gly Gly Arg Asp Arg Pro Asp Pro Glu Thr Asn Glu Trp Val
    290                       295                       300
Pro Ala His Phe Asp Ser Ser Ala Val Glu Asn Met Lys Arg Leu Ser
305                       310                       315                   320
Asp Ile Val Arg Val Pro Ala His Leu His Ala Leu Ser Leu Leu Cys
                325                       330                       335
Phe Glu Ile Met Pro Pro Pro Val Gln Val Gln Lys Glu Leu Gly Glu
            340                       345                       350
Arg Arg Ala Val Gly Phe Ser Gly Val Gly Leu Ala Val Ser Glu Gln
        355                       360                       365
Leu Asp Tyr Asp Ser Ile Ala Lys Leu Val Asp Asp Ser Lys Asn Ala
    370                       375                       380
Lys Asp Ala Phe Ser Asp Ala Ala Trp Ser Glu Val Asn Asp Met Tyr
385                       390                       395                   400
Asn Val Leu Lys Glu Ala Ile Tyr Gly Asp Gln Gly Cys Ala Val Ser
                405                       410                       415
Thr Asp Ser Leu Arg Leu Glu Gln Pro Trp Phe Asp Gly Ser Arg Arg
            420                       425                       430
Thr Asp
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<210> 24

```
<211>  444
<212>  DNA
<213>  Physcomitrella patens

<220>
<221>  CDS
<222>  (1)..(444)
<223>  GPAT/LPAAT

<400>  24
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atg atc cgg att ttc aga ggg caa cca tct gtg gtt cat gtg cac gtg      48
Met Ile Arg Ile Phe Arg Gly Gln Pro Ser Val Val His Val His Val
1               5                   10                  15
agg cgg gtc cct atg tct gat ctg cct gag gga gcc aac gcg att tct      96
Arg Arg Val Pro Met Ser Asp Leu Pro Glu Gly Ala Asn Ala Ile Ser
            20                  25                  30
aaa tgg tgt cac gat gcc ttt cac atc aag gac gat cgg ctg gag cag     144
Lys Trp Cys His Asp Ala Phe His Ile Lys Asp Asp Arg Leu Glu Gln
        35                  40                  45
cac gaa aaa gag aat acg ttt ggg gag gac ttg tat att cct att gaa     192
His Glu Lys Glu Asn Thr Phe Gly Glu Asp Leu Tyr Ile Pro Ile Glu
        50                  55                  60
cgg cca ctt aaa cct ctt att att gtg atc tcc tgg gcc atc act ttg     240
Arg Pro Leu Lys Pro Leu Ile Ile Val Ile Ser Trp Ala Ile Thr Leu
65                  70                  75                  80
ctg gct gca gca tgg tgg ttt cta aga cga gtt tta tcc act tgg aaa     288
Leu Ala Ala Ala Trp Trp Phe Leu Arg Arg Val Leu Ser Thr Trp Lys
                85                  90                  95
gga atc gcc tgg gtg gca gga gta ctc gtg gtc gtc atg ctg tgt gtc     336
Gly Ile Ala Trp Val Ala Gly Val Leu Val Val Val Met Leu Cys Val
                100                 105                 110
cag att tta gtg atg tcg tca caa tcg gaa aga agt tca gat cct gca     384
Gln Ile Leu Val Met Ser Ser Gln Ser Glu Arg Ser Ser Asp Pro Ala
            115                 120                 125
gct aag aag gcc aat caa aaa cag gcg gct tct gtt gct cac ctc ggc     432
Ala Lys Lys Ala Asn Gln Lys Gln Ala Ala Ser Val Ala His Leu Gly
    130                 135                 140
aaa acg gac tga                                                     444
Lys Thr Asp
145
```

```
<210>  25

<211>  147
<212>  PRT
<213>  Physcomitrella patens

<400>  25
```

```
Met Ile Arg Ile Phe Arg Gly Gln Pro Ser Val Val His Val His Val
1               5                   10                  15
Arg Arg Val Pro Met Ser Asp Leu Pro Glu Gly Ala Asn Ala Ile Ser
            20                  25                  30
Lys Trp Cys His Asp Ala Phe His Ile Lys Asp Asp Arg Leu Glu Gln
        35                  40                  45
```

```
His Glu Lys Glu Asn Thr Phe Gly Glu Asp Leu Tyr Ile Pro Ile Glu
    50                  55                  60
Arg Pro Leu Lys Pro Leu Ile Ile Val Ile Ser Trp Ala Ile Thr Leu
65                  70                  75                  80
Leu Ala Ala Ala Trp Trp Phe Leu Arg Arg Val Leu Ser Thr Trp Lys
                85                  90                  95
Gly Ile Ala Trp Val Ala Gly Val Leu Val Val Val Met Leu Cys Val
                100                 105                 110
Gln Ile Leu Val Met Ser Ser Gln Ser Glu Arg Ser Ser Asp Pro Ala
        115                 120                 125
Ala Lys Lys Ala Asn Gln Lys Gln Ala Ala Ser Val Ala His Leu Gly
        130                 135                 140
Lys Thr Asp
145


<210>   26

<211>   1710
<212>   DNA
<213>   Physcomitrella patens

<220>
<221>   CDS
<222>   (246)..(1394)
<223>   GPAT/LPAAT


<400>   26

gaattcgccc tttctctttt tcgtgctgct ccagccgata ttcatgacct gcccgggcag        60
gtcacattgc gtgttggcca tgtcctggtt gcagctctcg tgaccctcac gctcgcgagc       120
ggcaccgctc gtcttctgcc tcttgcttgc tcttgcttgc tttctgagga acagccccag       180
ctccggcacc agcataaggt cgtgtaggga gagagagaga gggggagaga agtaagcttg       240
gagtc atg gag ggc ggg ggc tcc ata atc gct ctt cct ctg ggg ctt atg      290
      Met Glu Gly Gly Gly Ser Ile Ile Ala Leu Pro Leu Gly Leu Met
      1               5                   10                  15
ttc ctc ttc tcc ggg ttc ttt atc aat atc ctg cag ctg ctg tcg gtg      338
Phe Leu Phe Ser Gly Phe Phe Ile Asn Ile Leu Gln Leu Leu Ser Val
                20                  25                  30
tta ttc att ttg ccg ttt tcg agg agg gcg tac cga gta gtg aat atg      386
Leu Phe Ile Leu Pro Phe Ser Arg Arg Ala Tyr Arg Val Val Asn Met
            35                  40                  45
att atg atg gag gtg ctg tgg tcg gag ctt ata tgg ctg ctg gat tgg      434
Ile Met Met Glu Val Leu Trp Ser Glu Leu Ile Trp Leu Leu Asp Trp
        50                  55                  60
tgg gcg aat gtg aag gtg aag gtt tac acg cca aag gag tcg tgg gag      482
Trp Ala Asn Val Lys Val Lys Val Tyr Thr Pro Lys Glu Ser Trp Glu
65                  70                  75
cac tta gga aag gag cac gca tta ctc att tgt aat cac cgc agt gac      530
His Leu Gly Lys Glu His Ala Leu Leu Ile Cys Asn His Arg Ser Asp
80                  85                  90                  95
ata gat tgg ctc gta gga tgg att att gcc cag aga ttg ggg tgt cta      578
Ile Asp Trp Leu Val Gly Trp Ile Ile Ala Gln Arg Leu Gly Cys Leu
                100                 105                 110
ggt ggg act cga gct gtt atg aag aag tcc acc aaa ttt ctt ccg gtc      626
Gly Gly Thr Arg Ala Val Met Lys Lys Ser Thr Lys Phe Leu Pro Val
                115                 120                 125
att ggc tgg tct atg tgg ttt tca gag tat gtg ttt tta tca aga gat      674
```

```
Ile Gly Trp Ser Met Trp Phe Ser Glu Tyr Val Phe Leu Ser Arg Asp
    130                 135                 140
tgg gcc aaa gat gag aag gtc ttg aag aat ggt tat tca agt ctt aag       722
Trp Ala Lys Asp Glu Lys Val Leu Lys Asn Gly Tyr Ser Ser Leu Lys
    145                 150                 155
ggc ttc ccc agg acc ttg tgg gtg gct ctt ttt gtg gaa ggc act cga       770
Gly Phe Pro Arg Thr Leu Trp Val Ala Leu Phe Val Glu Gly Thr Arg
160                 165                 170                 175
ttt acg aag gcc aaa ctt gag gct gcc caa aaa ttt gca gcg gat aca       818
Phe Thr Lys Ala Lys Leu Glu Ala Ala Gln Lys Phe Ala Ala Asp Thr
                180                 185                 190
ggg cta cgt gtt cca agg cat gtg ctt gtt cct cgc aca aaa ggg ttc       866
Gly Leu Arg Val Pro Arg His Val Leu Val Pro Arg Thr Lys Gly Phe
                195                 200                 205
gtt tcg gct gtg gag aac ttg cgt gaa ttt gtt ccg gta gtt tat gac       914
Val Ser Ala Val Glu Asn Leu Arg Glu Phe Val Pro Val Val Tyr Asp
                210                 215                 220
atg acc gtt gct ata tct aaa gag ctg ccc aat cct aca atg atc cgg       962
Met Thr Val Ala Ile Ser Lys Glu Leu Pro Asn Pro Thr Met Ile Arg
    225                 230                 235
att ttc aga ggg caa cca tct gtg gtt cat gtg cac gtg aga cgg gtc      1010
Ile Phe Arg Gly Gln Pro Ser Val Val His Val His Val Arg Arg Val
240                 245                 250                 255
cct atg tct gat ctg cct gag gga gcc aac gcg att tct aaa tgg tgt      1058
Pro Met Ser Asp Leu Pro Glu Gly Ala Asn Ala Ile Ser Lys Trp Cys
                260                 265                 270
cac gat gcc ttt cac atc aag gac gat cgg ctg gag cag cac gaa aaa      1106
His Asp Ala Phe His Ile Lys Asp Asp Arg Leu Glu Gln His Glu Lys
                275                 280                 285
gag aat acg ttt ggg gag gac ttg tat att cct att gaa cgg cca ctt      1154
Glu Asn Thr Phe Gly Glu Asp Leu Tyr Ile Pro Ile Glu Arg Pro Leu
                290                 295                 300
aaa cct ctt att att gtg atc tcc tgg gcc atc act ttg ctg gct gca      1202
Lys Pro Leu Ile Ile Val Ile Ser Trp Ala Ile Thr Leu Leu Ala Ala
    305                 310                 315
gca tgg tgg ttt cta aga cga gtt tta tcc act tgg aaa gga atc gcc      1250
Ala Trp Trp Phe Leu Arg Arg Val Leu Ser Thr Trp Lys Gly Ile Ala
320                 325                 330                 335
tgg gtg gca gga gta ctc gtg gtc gtc atg ctg tgt gtc cag att tta      1298
Trp Val Ala Gly Val Leu Val Val Val Met Leu Cys Val Gln Ile Leu
                340                 345                 350
gtg atg tcg tca caa tcg gaa aga agt tca gat cct gca gct aag aag      1346
Val Met Ser Ser Gln Ser Glu Arg Ser Ser Asp Pro Ala Ala Lys Lys
                355                 360                 365
gcc aat caa aaa cag gcg gct tct gtt gct cac ctc ggc aaa acg gac      1394
Ala Asn Gln Lys Gln Ala Ala Ser Val Ala His Leu Gly Lys Thr Asp
                370                 375                 380
tgagaacttt tgctttaacg caatccaaga cttaggcgtg ctagtctcag ttacaattag      1454
cattcaggca ctccagatgt gtcaagaaat tttagttact ctagccaaga attgtttgac      1514
accttgtagt ccacctaatt tccttgaacg attaagagca gcggccatta gatgattcga      1574
tttggtttct tgatagtatc tggtaccttc ttcttcaagc attgtgtatt ccgcttcagc      1634
cattcctttt tttaagatgt attgcttctc gttcgagggt aggtcatttc tgatctaatt      1694
ttgaaagcac taattc                                                      1710
```

<210>   27

<211>   383

<212> PRT
<213> Physcomitrella patens

<400> 27

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Met Glu Gly Gly Gly Ser Ile Ile Ala Leu Pro Leu Gly Leu Met Phe
1               5                   10                  15
Leu Phe Ser Gly Phe Phe Ile Asn Ile Leu Gln Leu Leu Ser Val Leu
            20                  25                  30
Phe Ile Leu Pro Phe Ser Arg Arg Ala Tyr Arg Val Val Asn Met Ile
            35                  40                  45
Met Met Glu Val Leu Trp Ser Glu Leu Ile Trp Leu Leu Asp Trp Trp
        50                  55                  60
Ala Asn Val Lys Val Lys Val Tyr Thr Pro Lys Glu Ser Trp Glu His
65                  70                  75                  80
Leu Gly Lys Glu His Ala Leu Leu Ile Cys Asn His Arg Ser Asp Ile
                85                  90                  95
Asp Trp Leu Val Gly Trp Ile Ile Ala Gln Arg Leu Gly Cys Leu Gly
            100                 105                 110
Gly Thr Arg Ala Val Met Lys Lys Ser Thr Lys Phe Leu Pro Val Ile
            115                 120                 125
Gly Trp Ser Met Trp Phe Ser Glu Tyr Val Phe Leu Ser Arg Asp Trp
        130                 135                 140
Ala Lys Asp Glu Lys Val Leu Lys Asn Gly Tyr Ser Ser Leu Lys Gly
145                 150                 155                 160
Phe Pro Arg Thr Leu Trp Val Ala Leu Phe Val Glu Gly Thr Arg Phe
                165                 170                 175
Thr Lys Ala Lys Leu Glu Ala Ala Gln Lys Phe Ala Ala Asp Thr Gly
            180                 185                 190
Leu Arg Val Pro Arg His Val Leu Val Pro Arg Thr Lys Gly Phe Val
            195                 200                 205
Ser Ala Val Glu Asn Leu Arg Glu Phe Val Pro Val Val Tyr Asp Met
        210                 215                 220
Thr Val Ala Ile Ser Lys Glu Leu Pro Asn Pro Thr Met Ile Arg Ile
225                 230                 235                 240
Phe Arg Gly Gln Pro Ser Val Val His Val His Val Arg Arg Val Pro
                245                 250                 255
Met Ser Asp Leu Pro Glu Gly Ala Asn Ala Ile Ser Lys Trp Cys His
        260                 265                 270
Asp Ala Phe His Ile Lys Asp Asp Arg Leu Glu Gln His Glu Lys Glu
            275                 280                 285
Asn Thr Phe Gly Glu Asp Leu Tyr Ile Pro Ile Glu Arg Pro Leu Lys
        290                 295                 300
Pro Leu Ile Ile Val Ile Ser Trp Ala Ile Thr Leu Leu Ala Ala Ala
305                 310                 315                 320
Trp Trp Phe Leu Arg Arg Val Leu Ser Thr Trp Lys Gly Ile Ala Trp
                325                 330                 335
Val Ala Gly Val Leu Val Val Val Met Leu Cys Val Gln Ile Leu Val
            340                 345                 350
Met Ser Ser Gln Ser Glu Arg Ser Ser Asp Pro Ala Ala Lys Lys Ala
        355                 360                 365
Asn Gln Lys Gln Ala Ala Ser Val Ala His Leu Gly Lys Thr Asp
        370                 375                 380
```

<210> 28

<211> 628

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<212>   DNA
<213>   Cryptocodinium cohnii

<220>
<221>   CDS
<222>   (3)..(578)
<223>   DAGAT

<400>   28

tt gat gat tgg atc gcc gcg ttg gcg act gct tgt gca agc acg gat        47
   Asp Asp Trp Ile Ala Ala Leu Ala Thr Ala Cys Ala Ser Thr Asp
   1               5                   10                  15
ggg gtt acg gac gtc gac agc ctg aag ccc tca gca agt gca gtt ccc        95
Gly Val Thr Asp Val Asp Ser Leu Lys Pro Ser Ala Ser Ala Val Pro
                20                  25                  30
cat gga ccc ccc aag gcg aag gtc agt gag cta tcg gcc ctg cgc aag       143
His Gly Pro Pro Lys Ala Lys Val Ser Glu Leu Ser Ala Leu Arg Lys
                35                  40                  45
gtg cac aat cga aac cgg acc agc gtt ttg acc aac gag gac gga ggc       191
Val His Asn Arg Asn Arg Thr Ser Val Leu Thr Asn Glu Asp Gly Gly
        50                  55                  60
att cct gag tgc aac gtt gtg ggg atc gtg aac ctc tgt gtt act gtg       239
Ile Pro Glu Cys Asn Val Val Gly Ile Val Asn Leu Cys Val Thr Val
    65                  70                  75
atg gtc ttg atc cac ctg cgc ctc att tat gag agc atc cgg aag cac       287
Met Val Leu Ile His Leu Arg Leu Ile Tyr Glu Ser Ile Arg Lys His
80                  85                  90                  95
ggt gtt ttg ttg gac acc ttc cgg gtg gcg gcc cac acc gca ctc aag       335
Gly Val Leu Leu Asp Thr Phe Arg Val Ala Ala His Thr Ala Leu Lys
                100                 105                 110
cca ggt aac ttc cag tgt acg ctt tgt ttc ttc gct ttg ccg gtc ctg       383
Pro Gly Asn Phe Gln Cys Thr Leu Cys Phe Phe Ala Leu Pro Val Leu
                115                 120                 125
gcc atc ttg gcg acc ttc att gag gtc ttg gcg agc aag gga cag ttg       431
Ala Ile Leu Ala Thr Phe Ile Glu Val Leu Ala Ser Lys Gly Gln Leu
                130                 135                 140
ggg atc tcg ctt cgc gag cac cct gca tgc cgg gct ttg tac aat ctg       479
Gly Ile Ser Leu Arg Glu His Pro Ala Cys Arg Ala Leu Tyr Asn Leu
    145                 150                 155
cct tac cat ccc tgt cct ggt cat cca cca ctt tca ggc aac tcc tct       527
Pro Tyr His Pro Cys Pro Gly His Pro Pro Leu Ser Gly Asn Ser Ser
160                 165                 170                 175
cgt ggg agc ctc gtt gct gat tgc tgc gac cac tct ctt ctt gaa agt       575
Arg Gly Ser Leu Val Ala Asp Cys Cys Asp His Ser Leu Leu Glu Ser
                180                 185                 190
tgg tgagcttcgc ccacgtgaat tggctctcgg cgacagtgga aggcgatgga          628
Trp


<210>   29

<211>   192
<212>   PRT

<213>   Cryptocodinium cohnii
```

<400> 29

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Asp Asp Trp Ile Ala Ala Leu Ala Thr Ala Cys Ala Ser Thr Asp Gly
1               5                   10                  15
Val Thr Asp Val Asp Ser Leu Lys Pro Ser Ala Ser Ala Val Pro His
            20                  25                  30
Gly Pro Pro Lys Ala Lys Val Ser Glu Leu Ser Ala Leu Arg Lys Val
        35                  40                  45
His Asn Arg Asn Arg Thr Ser Val Leu Thr Asn Glu Asp Gly Gly Ile
    50                  55                  60
Pro Glu Cys Asn Val Val Gly Ile Val Asn Leu Cys Val Thr Val Met
65                  70                  75                  80
Val Leu Ile His Leu Arg Leu Ile Tyr Glu Ser Ile Arg Lys His Gly
                85                  90                  95
Val Leu Leu Asp Thr Phe Arg Val Ala Ala His Thr Ala Leu Lys Pro
            100                 105                 110
Gly Asn Phe Gln Cys Thr Leu Cys Phe Phe Ala Leu Pro Val Leu Ala
        115                 120                 125
Ile Leu Ala Thr Phe Ile Glu Val Leu Ala Ser Lys Gly Gln Leu Gly
        130                 135                 140
Ile Ser Leu Arg Glu His Pro Ala Cys Arg Ala Leu Tyr Asn Leu Pro
145                 150                 155                 160
Tyr His Pro Cys Pro Gly His Pro Pro Leu Ser Gly Asn Ser Ser Arg
                165                 170                 175
Gly Ser Leu Val Ala Asp Cys Cys Asp His Ser Leu Leu Glu Ser Trp
            180                 185                 190
```

<210> 30

<211> 1272
<212> DNA
<213> Cryptocodinium cohnii

<220>
<221> CDS
<222> (164)..(1120)
<223> DAGAT

<400> 30

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ggacactgac atggactgaa ggagtagaaa gccgtagcca ttttggctca agctccagtg      60
aacagtcgcg ccctgactgc agaggggtgc ggcacaaacc ctcagataca cacacatccc     120
gtgagtttat agattcttgt ctcgcgctct tcttgtgcaa gcg atg gct gga aag     175
                                                  Met Ala Gly Lys
                                                  1
tgg atg ctg ctc agt ggt ggt gca gca gct gca gcg ttg gcg ctt ctg     223
Trp Met Leu Leu Ser Gly Gly Ala Ala Ala Ala Ala Leu Ala Leu Leu
5               10                  15                  20
gag ggc acc cag ctt cga gcg tcg aca tcg gca cgc gcc cgg ata ttg     271
Glu Gly Thr Gln Leu Arg Ala Ser Thr Ser Ala Arg Ala Arg Ile Leu
            25                  30                  35
ctg gtt tcg ttg gca gca tat ctc cca acg tac ctc gat gga agc gag     319
Leu Val Ser Leu Ala Ala Tyr Leu Pro Thr Tyr Leu Asp Gly Ser Glu
        40                  45                  50
tac cgg gct gcc cct cga cga agc gag cga gcc tca cgg gtc ctg cgg     367
Tyr Arg Ala Ala Pro Arg Arg Ser Glu Arg Ala Ser Arg Val Leu Arg
        55                  60                  65
```

```
cag ttg tac aaa gtc atg gta aat tgg ttc ttc aca atc aaa cgg cca      415
Gln Leu Tyr Lys Val Met Val Asn Trp Phe Phe Thr Ile Lys Arg Pro
    70              75                  80
gta atc gag gct tcc gaa gag ctg aca gct tgt gac cag tgc atc ttg      463
Val Ile Glu Ala Ser Glu Glu Leu Thr Ala Cys Asp Gln Cys Ile Leu
85              90                  95                  100
gcg gtc cat ccc cat gga gta cct tct ctc gac cat ttg ctg acg gtc      511
Ala Val His Pro His Gly Val Pro Ser Leu Asp His Leu Leu Thr Val
            105             110                 115
atc gcc tat gat cct gac ttg gaa cgg gtg ttg ccc cag ttg cgg aga      559
Ile Ala Tyr Asp Pro Asp Leu Glu Arg Val Leu Pro Gln Leu Arg Arg
            120             125                 130
agt gcc ttg agt gca ggt gtc ctg ttc aag att ccc att ctg cgc gag      607
Ser Ala Leu Ser Ala Gly Val Leu Phe Lys Ile Pro Ile Leu Arg Glu
        135             140                 145
gtc ctt ctg tgg act ggc tgt gtc gac gct ggc ggg aag acc gtg gac      655
Val Leu Leu Trp Thr Gly Cys Val Asp Ala Gly Gly Lys Thr Val Asp
        150             155                 160
tct tgc ttg aag gct ggt ctc agc ctt tct gtt gtg ccc ggc ggc gaa      703
Ser Cys Leu Lys Ala Gly Leu Ser Leu Ser Val Val Pro Gly Gly Glu
165             170                 175                 180
cgc gag caa ctt ctc gca cag cga ggg aac aag gaa atc ctc gtg ctg      751
Arg Glu Gln Leu Leu Ala Gln Arg Gly Asn Lys Glu Ile Leu Val Leu
            185             190                 195
aaa cac agg aag ggc ttt gtc aag tac gcc ttg agg cat ggc att ccg      799
Lys His Arg Lys Gly Phe Val Lys Tyr Ala Leu Arg His Gly Ile Pro
            200             205                 210
ttg gta cct gtg tat tgc ttc ggc gag aac caa ctt ttt tgg cag tcc      847
Leu Val Pro Val Tyr Cys Phe Gly Glu Asn Gln Leu Phe Trp Gln Ser
        215             220                 225
tcc ttc ctc ttc aag gtt cgc agt tgg ctg cgg cgc act ctg gga gtg      895
Ser Phe Leu Phe Lys Val Arg Ser Trp Leu Arg Arg Thr Leu Gly Val
        230             235                 240
gcg ctc gtg ttg ccc tac gga ggc tgc tgc aat ctg cct ggt gtg ccc      943
Ala Leu Val Leu Pro Tyr Gly Gly Cys Cys Asn Leu Pro Gly Val Pro
245             250                 255                 260
ttc tcg gag ccg gtg cag ctc gtc gtc gga gct ccc ttg aag ctt ccg      991
Phe Ser Glu Pro Val Gln Leu Val Val Gly Ala Pro Leu Lys Leu Pro
            265             270                 275
aag atc gaa gag ccg agc gga gtg gaa ata gcc aag tgg cac gct cgg     1039
Lys Ile Glu Glu Pro Ser Gly Val Glu Ile Ala Lys Trp His Ala Arg
            280             285                 290
tac atg gag tgt ttg gaa gcc ttg ttc aag cgg cac cga gtt gaa gct     1087
Tyr Met Glu Cys Leu Glu Ala Leu Phe Lys Arg His Arg Val Glu Ala
            295             300                 305
gga tat cct gaa ttg gaa ctc gag ttc atc tga aggtttcaag tttacatgtg   1140
Gly Tyr Pro Glu Leu Glu Leu Glu Phe Ile
            310             315
tctcacagtc ctccgctctg agccccactc attgtagtta ctcttctatg tgtgcaacgt   1200
cgaccacagg agttaccgtc aaagacggtt gctccttgct gcttcgagag aaaaaaaaaa   1260
aaaaaaaaaa aa                                                       1272
```

<210> 31

<211> 318
<212> PRT
<213> Cryptocodinium cohnii

<400> 31

```
Met Ala Gly Lys Trp Met Leu Leu Ser Gly Gly Ala Ala Ala Ala
1               5               10              15
Leu Ala Leu Leu Glu Gly Thr Gln Leu Arg Ala Ser Thr Ser Ala Arg
            20              25              30
Ala Arg Ile Leu Leu Val Ser Leu Ala Ala Tyr Leu Pro Thr Tyr Leu
        35              40              45
Asp Gly Ser Glu Tyr Arg Ala Ala Pro Arg Arg Ser Glu Arg Ala Ser
    50              55              60
Arg Val Leu Arg Gln Leu Tyr Lys Val Met Val Asn Trp Phe Phe Thr
65              70              75              80
Ile Lys Arg Pro Val Ile Glu Ala Ser Glu Glu Leu Thr Ala Cys Asp
            85              90              95
Gln Cys Ile Leu Ala Val His Pro His Gly Val Pro Ser Leu Asp His
        100             105             110
Leu Leu Thr Val Ile Ala Tyr Asp Pro Asp Leu Glu Arg Val Leu Pro
        115             120             125
Gln Leu Arg Arg Ser Ala Leu Ser Ala Gly Val Leu Phe Lys Ile Pro
    130             135             140
Ile Leu Arg Glu Val Leu Leu Trp Thr Gly Cys Val Asp Ala Gly Gly
145             150             155             160
Lys Thr Val Asp Ser Cys Leu Lys Ala Gly Leu Ser Leu Ser Val Val
            165             170             175
Pro Gly Gly Glu Arg Glu Gln Leu Leu Ala Gln Arg Gly Asn Lys Glu
            180             185             190
Ile Leu Val Leu Lys His Arg Lys Gly Phe Val Lys Tyr Ala Leu Arg
        195             200             205
His Gly Ile Pro Leu Val Pro Val Tyr Cys Phe Gly Glu Asn Gln Leu
    210             215             220
Phe Trp Gln Ser Ser Phe Leu Phe Lys Val Arg Ser Trp Leu Arg Arg
225             230             235             240
Thr Leu Gly Val Ala Leu Val Leu Pro Tyr Gly Gly Cys Cys Asn Leu
            245             250             255
Pro Gly Val Pro Phe Ser Glu Pro Val Gln Leu Val Val Gly Ala Pro
            260             265             270
Leu Lys Leu Pro Lys Ile Glu Glu Pro Ser Gly Val Glu Ile Ala Lys
        275             280             285
Trp His Ala Arg Tyr Met Glu Cys Leu Glu Ala Leu Phe Lys Arg His
    290             295             300
Arg Val Glu Ala Gly Tyr Pro Glu Leu Glu Leu Glu Phe Ile
305             310             315
```

<210> 32

<211> 448
<212> DNA
<213> Cryptocodinium cohnii

<220>
<221> CDS
<222> (1)..(426)
<223> DAGAT

<400> 32

```
atc aag atg gtg ccg ttt ttg aag aac gtg ctg ggg ctc ttt ggg ctg      48
```

```
      Ile Lys Met Val Pro Phe Leu Lys Asn Val Leu Gly Leu Phe Gly Leu
      1               5                   10                  15
      atc gac gcg agc aag cag gtg ttg gtc aag cga ttg aag cgc cca ggt       96
      Ile Asp Ala Ser Lys Gln Val Leu Val Lys Arg Leu Lys Arg Pro Gly
                      20                  25                  30
      ggt tcc ctg gtg att tac atc gga ggg atg gtg gag ctc ttc atg tcc      144
      Gly Ser Leu Val Ile Tyr Ile Gly Gly Met Val Glu Leu Phe Met Ser
                  35                  40                  45
      agc ccc aag cag gaa gtc gtc ttc ttg aag aag agg aag ggt ttt atc      192
      Ser Pro Lys Gln Glu Val Val Phe Leu Lys Lys Arg Lys Gly Phe Ile
              50                  55                  60
      cga ctc gct ctg agc aca ggt gcc gat gtc gtg ccg atc tac ttg ttc      240
      Arg Leu Ala Leu Ser Thr Gly Ala Asp Val Val Pro Ile Tyr Leu Phe
      65                  70                  75                  80
      ggc aac acc acc gtg ctc tca gtg ctg acc gct ggc cct ctg gcc tct      288
      Gly Asn Thr Thr Val Leu Ser Val Leu Thr Ala Gly Pro Leu Ala Ser
                          85                  90                  95
      ctg agc cgt gcc gcc ggg gtg tca gtg acc att ttt tgg gga cgc ttc      336
      Leu Ser Arg Ala Ala Gly Val Ser Val Thr Ile Phe Trp Gly Arg Phe
                      100                 105                 110
      ggc ttg ccg atg ccc tac ccc gtc aag ctc acc tat gcc cgt ggc cgt      384
      Gly Leu Pro Met Pro Tyr Pro Val Lys Leu Thr Tyr Ala Arg Gly Arg
                  115                 120                 125
      ccc atc ggt ctc cct cat atc gaa atc cta cag atg aga cat             426
      Pro Ile Gly Leu Pro His Ile Glu Ile Leu Gln Met Arg His
              130                 135                 140
      tgaccgttgg catgacgtgt ac                                           448
```

<210> 33

<211> 142
<212> PRT
<213> Cryptocodinium cohnii

<400> 33

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      Ile Lys Met Val Pro Phe Leu Lys Asn Val Leu Gly Leu Phe Gly Leu
      1               5                   10                  15
      Ile Asp Ala Ser Lys Gln Val Leu Val Lys Arg Leu Lys Arg Pro Gly
                      20                  25                  30
      Gly Ser Leu Val Ile Tyr Ile Gly Gly Met Val Glu Leu Phe Met Ser
                  35                  40                  45
      Ser Pro Lys Gln Glu Val Val Phe Leu Lys Lys Arg Lys Gly Phe Ile
              50                  55                  60
      Arg Leu Ala Leu Ser Thr Gly Ala Asp Val Val Pro Ile Tyr Leu Phe
      65                  70                  75                  80
      Gly Asn Thr Thr Val Leu Ser Val Leu Thr Ala Gly Pro Leu Ala Ser
                          85                  90                  95
      Leu Ser Arg Ala Ala Gly Val Ser Val Thr Ile Phe Trp Gly Arg Phe
                      100                 105                 110
      Gly Leu Pro Met Pro Tyr Pro Val Lys Leu Thr Tyr Ala Arg Gly Arg
                  115                 120                 125
      Pro Ile Gly Leu Pro His Ile Glu Ile Leu Gln Met Arg His
              130                 135                 140
```

<210> 34

```
<211>    1757
<212>    DNA
<213>    Physcomitrella patens

<220>
<221>    CDS
<222>    (76)..(1578)
<223>    LCAT


<400>    34

ggcgcgccag aggacgagac aaggggggact tgtgagaatc ttcgagcttc aacctgtcaa        60
gcttcggtct ccacc atg tgt tca att tct tgt gga tcc act ccg cag caa       111
               Met Cys Ser Ile Ser Cys Gly Ser Thr Pro Gln Gln
                1               5                   10
ctc tgt cat tac agg aag agc ggg gag ctg att aca aga aag agt cgc       159
Leu Cys His Tyr Arg Lys Ser Gly Glu Leu Ile Thr Arg Lys Ser Arg
         15               20                  25
gca gct att cgg tgg tgg agg tat ggc caa caa tgc aag gtg ctg ttg       207
Ala Ala Ile Arg Trp Trp Arg Tyr Gly Gln Gln Cys Lys Val Leu Leu
     30               35                  40
ccg ttg gat ttg att cga tca tcg tct caa ttc ttc atc gta gtt ctc       255
Pro Leu Asp Leu Ile Arg Ser Ser Ser Gln Phe Phe Ile Val Val Leu
45               50                  55                      60
act ctg acg ctc ttc ctg ttc acc acg tgt gga gct gtg cat act gcg       303
Thr Leu Thr Leu Phe Leu Phe Thr Thr Cys Gly Ala Val His Thr Ala
             65                  70                  75
gca caa gac aga tca ttc gca aca ttg agc caa aga tca aga gcg tct       351
Ala Gln Asp Arg Ser Phe Ala Thr Leu Ser Gln Arg Ser Arg Ala Ser
         80                  85                  90
ctc ttc agt gtg gga cgg gca caa gca agg aac aaa cac cat ttg gcg       399
Leu Phe Ser Val Gly Arg Ala Gln Ala Arg Asn Lys His His Leu Ala
         95                  100                 105
ccg gtg gtc ata gtt cca ggc acc ggc ggg aat caa cta gag gcc agg       447
Pro Val Val Ile Val Pro Gly Thr Gly Gly Asn Gln Leu Glu Ala Arg
     110                 115                 120
ttg aca gct gat tac gag gct aac aag cca tgg tgc tac agc ttc aga       495
Leu Thr Ala Asp Tyr Glu Ala Asn Lys Pro Trp Cys Tyr Ser Phe Arg
125                 130                 135                 140
aaa gat tac ttc agg ttg tgg ctg gat gtg aaa aca ctg ttt cca cct       543
Lys Asp Tyr Phe Arg Leu Trp Leu Asp Val Lys Thr Leu Phe Pro Pro
                 145                 150                 155
ttc acg acg tgt ttc gcc gac cgc ctg agc ttg gac tac aac ccg cag       591
Phe Thr Thr Cys Phe Ala Asp Arg Leu Ser Leu Asp Tyr Asn Pro Gln
             160                 165                 170
tcc gat gcc tat agc aac atc aag ggc gtg aag acg cgg gta ccg ttt       639
Ser Asp Ala Tyr Ser Asn Ile Lys Gly Val Lys Thr Arg Val Pro Phe
         175                 180                 185
ttt ggt act acc gaa gga atg gag tac ctg gat ccc tca ctc aaa ttc       687
Phe Gly Thr Thr Glu Gly Met Glu Tyr Leu Asp Pro Ser Leu Lys Phe
     190                 195                 200
ttg aca ggc tac atg ata cac ttg gtg aac gca tta aaa gct cat ggt       735
Leu Thr Gly Tyr Met Ile His Leu Val Asn Ala Leu Lys Ala His Gly
205                 210                 215                 220
tac gag aac gga aag tca tta tac gga gct cca tac gac ttt cgg ttc       783
Tyr Glu Asn Gly Lys Ser Leu Tyr Gly Ala Pro Tyr Asp Phe Arg Phe
             225                 230                 235
```

```
gca ccg ggg cca cat gca tcc aac gta gct cta gag tac ctg aaa gac        831
Ala Pro Gly Pro His Ala Ser Asn Val Ala Leu Glu Tyr Leu Lys Asp
            240                 245                 250
ctg aaa gat ctc ata gaa acc gcg tac tca gta aat gcc aac gag ccg        879
Leu Lys Asp Leu Ile Glu Thr Ala Tyr Ser Val Asn Ala Asn Glu Pro
            255                 260                 265
gtg gtc atc ctc gct cac agc atg ggc ggg ttg tgg act ctc ttc ttc        927
Val Val Ile Leu Ala His Ser Met Gly Gly Leu Trp Thr Leu Phe Phe
            270                 275                 280
ctg aac cag caa tcc atg gag tgg agg aac aaa tac gtt tcc cgc ttt        975
Leu Asn Gln Gln Ser Met Glu Trp Arg Asn Lys Tyr Val Ser Arg Phe
285                 290                 295                 300
gtg tct gta gct acc ccg tgg gga ggg gcg gtc gaa cag atg atg acc       1023
Val Ser Val Ala Thr Pro Trp Gly Gly Ala Val Glu Gln Met Met Thr
                305                 310                 315
ttc gca tcc ggc aat ccg gag gga gtt ccc ttt gtg aac tcc ctg gtc       1071
Phe Ala Ser Gly Asn Pro Glu Gly Val Pro Phe Val Asn Ser Leu Val
                320                 325                 330
gtg cgc gaa gag cag cgg cgc tca gag tct aac ttg tgg ctg ctg cca       1119
Val Arg Glu Glu Gln Arg Arg Ser Glu Ser Asn Leu Trp Leu Leu Pro
            335                 340                 345
gtg cgg cgc tgc ttc aga gac cga cca ttg gta att acc tcg tcg cgc       1167
Val Arg Arg Cys Phe Arg Asp Arg Pro Leu Val Ile Thr Ser Ser Arg
            350                 355                 360
aac tac aca gct ggg gac atg gaa cag ttt ctg tgc gac atc ggt ttc       1215
Asn Tyr Thr Ala Gly Asp Met Glu Gln Phe Leu Cys Asp Ile Gly Phe
365                 370                 375                 380
cct gaa ggg gtc gcg cca tac aaa tcc cgg ata ccg cac cta acg gac      ·1263
Pro Glu Gly Val Ala Pro Tyr Lys Ser Arg Ile Pro His Leu Thr Asp
                385                 390                 395
att cta caa cct cct caa gtc ccc gtc acc cta att cac ggc tat ggc       1311
Ile Leu Gln Pro Pro Gln Val Pro Val Thr Leu Ile His Gly Tyr Gly
                400                 405                 410
gtg ccg acg gcg gag aca cta agc tac gag aag aag gga ttc gac aac       1359
Val Pro Thr Ala Glu Thr Leu Ser Tyr Glu Lys Lys Gly Phe Asp Asn
            415                 420                 425·
cat ccc gaa atc aca gaa ggt gat ggc gac ggg acg gtg aat gtg tgc       1407
His Pro Glu Ile Thr Glu Gly Asp Gly Asp Gly Thr Val Asn Val Cys
            430                 435                 440
agc ttg acc gcg gtg gtt gag gaa tgg gag cga gtc gca ggt cag gag       1455
Ser Leu Thr Ala Val Val Glu Glu Trp Glu Arg Val Ala Gly Gln Glu
445                 450                 455                 460
ttg gaa atg att gcg ctg cat ggc aaa caa cat atg caa atc ttg cac       1503
Leu Glu Met Ile Ala Leu His Gly Lys Gln His Met Gln Ile Leu His
                465                 470                 475
gac gac cat tct gtg caa gtg atc gtg gac gcc att ctc aat gtt acc       1551
Asp Asp His Ser Val Gln Val Ile Val Asp Ala Ile Leu Asn Val Thr
                480                 485                 490
cca cag gaa cag ctt atg ttc cac taa gccctaatcg taaccctaaa            1598
Pro Gln Glu Gln Leu Met Phe His
                495                 500
cctagctcca atcctcacag gatcaggcca cattctcctt gaaaaacagc ataaggtcga    1658
ttctccgcag cctctcttcc attccacctc cccctttgta tctctctcca ttcaattgta    1718
caattgtttt tttattcaaa aaaaaaaaaa aaaaaaaaa                           1757
```

<210> 35

<211> 500
<212> PRT
<213> Physcomitrella patens

<400> 35

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Met Cys Ser Ile Ser Cys Gly Ser Thr Pro Gln Gln Leu Cys His Tyr
1               5                   10                  15
Arg Lys Ser Gly Glu Leu Ile Thr Arg Lys Ser Arg Ala Ala Ile Arg
            20                  25                  30
Trp Trp Arg Tyr Gly Gln Gln Cys Lys Val Leu Leu Pro Leu Asp Leu
            35                  40                  45
Ile Arg Ser Ser Ser Gln Phe Phe Ile Val Val Leu Thr Leu Thr Leu
        50                  55                  60
Phe Leu Phe Thr Thr Cys Gly Ala Val His Thr Ala Ala Gln Asp Arg
65                  70                  75                  80
Ser Phe Ala Thr Leu Ser Gln Arg Ser Arg Ala Ser Leu Phe Ser Val
                85                  90                  95
Gly Arg Ala Gln Ala Arg Asn Lys His His Leu Ala Pro Val Val Ile
            100                 105                 110
Val Pro Gly Thr Gly Gly Asn Gln Leu Glu Ala Arg Leu Thr Ala Asp
            115                 120                 125
Tyr Glu Ala Asn Lys Pro Trp Cys Tyr Ser Phe Arg Lys Asp Tyr Phe
        130                 135                 140
Arg Leu Trp Leu Asp Val Lys Thr Leu Phe Pro Pro Phe Thr Thr Cys
145                 150                 155                 160
Phe Ala Asp Arg Leu Ser Leu Asp Tyr Asn Pro Gln Ser Asp Ala Tyr
                165                 170                 175
Ser Asn Ile Lys Gly Val Lys Thr Arg Val Pro Phe Phe Gly Thr Thr
            180                 185                 190
Glu Gly Met Glu Tyr Leu Asp Pro Ser Leu Lys Phe Leu Thr Gly Tyr
            195                 200                 205
Met Ile His Leu Val Asn Ala Leu Lys Ala His Gly Tyr Glu Asn Gly
        210                 215                 220
Lys Ser Leu Tyr Gly Ala Pro Tyr Asp Phe Arg Phe Ala Pro Gly Pro
225                 230                 235                 240
His Ala Ser Asn Val Ala Leu Glu Tyr Leu Lys Asp Leu Lys Asp Leu
                245                 250                 255
Ile Glu Thr Ala Tyr Ser Val Asn Ala Asn Glu Pro Val Val Ile Leu
            260                 265                 270
Ala His Ser Met Gly Gly Leu Trp Thr Leu Phe Phe Leu Asn Gln Gln
        275                 280                 285
Ser Met Glu Trp Arg Asn Lys Tyr Val Ser Arg Phe Val Ser Val Ala
        290                 295                 300
Thr Pro Trp Gly Gly Ala Val Glu Gln Met Met Thr Phe Ala Ser Gly
305                 310                 315                 320
Asn Pro Glu Gly Val Pro Phe Val Asn Ser Leu Val Val Arg Glu Glu
                325                 330                 335
Gln Arg Arg Ser Glu Ser Asn Leu Trp Leu Leu Pro Val Arg Arg Cys
            340                 345                 350
Phe Arg Asp Arg Pro Leu Val Ile Thr Ser Ser Arg Asn Tyr Thr Ala
        355                 360                 365
Gly Asp Met Glu Gln Phe Leu Cys Asp Ile Gly Phe Pro Glu Gly Val
        370                 375                 380
Ala Pro Tyr Lys Ser Arg Ile Pro His Leu Thr Asp Ile Leu Gln Pro
385                 390                 395                 400
Pro Gln Val Pro Val Thr Leu Ile His Gly Tyr Gly Val Pro Thr Ala
```

```
                    405                    410                    415
Glu Thr Leu Ser Tyr Glu Lys Lys Gly Phe Asp Asn His Pro Glu Ile
            420                    425                    430
Thr Glu Gly Asp Gly Asp Gly Thr Val Asn Val Cys Ser Leu Thr Ala
        435                    440                    445
Val Val Glu Glu Trp Glu Arg Val Ala Gly Gln Glu Leu Glu Met Ile
        450                    455                    460
Ala Leu His Gly Lys Gln His Met Gln Ile Leu His Asp Asp His Ser
465                    470                    475                    480
Val Gln Val Ile Val Asp Ala Ile Leu Asn Val Thr Pro Gln Glu Gln
                485                    490                    495
Leu Met Phe His
            500
```

```
<210>   36

<211>   1893
<212>   DNA
<213>   Fusarium graminaeum

<220>
<221>   CDS
<222>   (1)..(1893)
<223>   LCAT

<400>   36

atg gga aag tcc act tta cga cgc cgg aat ggc caa gat gcg aca aat         48
Met Gly Lys Ser Thr Leu Arg Arg Arg Asn Gly Gln Asp Ala Thr Asn
1                   5                  10                  15
aac gat agc gcc gac gct gac gac act ccg aga gaa gaa agc cca acg         96
Asn Asp Ser Ala Asp Ala Asp Asp Thr Pro Arg Glu Glu Ser Pro Thr
                20                  25                  30
gct gag ccg acc aca cac gtt cga gtt gtt caa cac gcc gtg ccc aga        144
Ala Glu Pro Thr Thr His Val Arg Val Val Gln His Ala Val Pro Arg
            35                  40                  45
acc cga aaa cgc cgc aac acc ttc gtc ttc ttc ctt ggt agt ttg ttt        192
Thr Arg Lys Arg Arg Asn Thr Phe Val Phe Phe Leu Gly Ser Leu Phe
        50                  55                  60
gga att ata gcc gcc gga ttt ttc gct tcc agc aat gat ctt att gac        240
Gly Ile Ile Ala Ala Gly Phe Phe Ala Ser Ser Asn Asp Leu Ile Asp
65                  70                  75                  80
ctc ccc gag ttt acc gac ttg tcg atg gat aac ttg atg gat gtt ctg        288
Leu Pro Glu Phe Thr Asp Leu Ser Met Asp Asn Leu Met Asp Val Leu
                85                  90                  95
cct gcc ggc ttg ata aag gac atg cgc gac ctt gtt cag ggc gag cgg        336
Pro Ala Gly Leu Ile Lys Asp Met Arg Asp Leu Val Gln Gly Glu Arg
            100                 105                 110
gac att gcc gaa tcg tac gag cca ttc tct gtt ggc gaa aag gct cga        384
Asp Ile Ala Glu Ser Tyr Glu Pro Phe Ser Val Gly Glu Lys Ala Arg
            115                 120                 125
tcc gag ggt cta gga gtt cac cat cct atg atc atg ata cct ggt gtt        432
Ser Glu Gly Leu Gly Val His His Pro Met Ile Met Ile Pro Gly Val
        130                 135                 140
atc tca act gga ctc gaa tcg tgg ggt acg gct aat atc tcg aaa ccc        480
Ile Ser Thr Gly Leu Glu Ser Trp Gly Thr Ala Asn Ile Ser Lys Pro
145                 150                 155                 160
```

```
tac ttt aga aaa cga ctt tgg ggt agt tgg aca atg atg aga gct ctg      528
Tyr Phe Arg Lys Arg Leu Trp Gly Ser Trp Thr Met Met Arg Ala Leu
            165             170                 175
gtt atg gac aag gag gtt tgg aag aag cac gtc atg ctc gac aag agg      576
Val Met Asp Lys Glu Val Trp Lys Lys His Val Met Leu Asp Lys Arg
            180             185                 190
acg ggc ctt gac ccg cct gac gta aag ttg agg gct gcc caa ggg ttc      624
Thr Gly Leu Asp Pro Pro Asp Val Lys Leu Arg Ala Ala Gln Gly Phe
            195             200                 205
gat gcg acc gat ttc ttc atc acg gga tat tgg atc tgg agc aaa atc      672
Asp Ala Thr Asp Phe Phe Ile Thr Gly Tyr Trp Ile Trp Ser Lys Ile
            210             215                 220
ttt gag aat ctc gca tcc atc ggc tac gac cca acg aac tcg ttc acg      720
Phe Glu Asn Leu Ala Ser Ile Gly Tyr Asp Pro Thr Asn Ser Phe Thr
225             230             235                 240
gct gct tac gat tgg cgc ttg tcg tat ccc aac ctt gag gta cgg gac      768
Ala Ala Tyr Asp Trp Arg Leu Ser Tyr Pro Asn Leu Glu Val Arg Asp
                245             250                 255
cgc tac ttc act cgg cta aag tcg cat atc gaa atc gcg gtg gcc act      816
Arg Tyr Phe Thr Arg Leu Lys Ser His Ile Glu Ile Ala Val Ala Thr
            260             265                 270
gag gac aaa aaa gtc gtc ctc gca tca cac agt atg ggg agc caa gtc      864
Glu Asp Lys Lys Val Val Leu Ala Ser His Ser Met Gly Ser Gln Val
            275             280                 285
ctt tac tat ttt ctc cac tgg gtg cag tca gaa aga ggc gga cgc ggt      912
Leu Tyr Tyr Phe Leu His Trp Val Gln Ser Glu Arg Gly Gly Arg Gly
            290             295                 300
ggg ccg gat tgg gtt gag cgt cac att gac gcc tgg atc aac atc agc      960
Gly Pro Asp Trp Val Glu Arg His Ile Asp Ala Trp Ile Asn Ile Ser
305             310             315                 320
gga tgc atg ctt gga gca gtc aag gat ttg acc gct gtg ctc tcc ggc     1008
Gly Cys Met Leu Gly Ala Val Lys Asp Leu Thr Ala Val Leu Ser Gly
                325             330                 335
gag atg cgc gac aca gct caa ctg aac ccg ttc gct att tac ggc ctg     1056
Glu Met Arg Asp Thr Ala Gln Leu Asn Pro Phe Ala Ile Tyr Gly Leu
            340             345                 350
gaa aag ttc ttg agt aaa gag gag aga gcc gag atc ttt cgc ggc atg     1104
Glu Lys Phe Leu Ser Lys Glu Glu Arg Ala Glu Ile Phe Arg Gly Met
            355             360                 365
ccc ggg ata tcc tcc atg ttg ccc atc ggc ggc aac tct gta tgg ggt     1152
Pro Gly Ile Ser Ser Met Leu Pro Ile Gly Gly Asn Ser Val Trp Gly
            370             375                 380
aac ttg acc tgg gct cca gac gac ttg cca ggc cag aac cgt tca tat     1200
Asn Leu Thr Trp Ala Pro Asp Asp Leu Pro Gly Gln Asn Arg Ser Tyr
385             390             395                 400
gga tct ctc ttg aac ttt agg gtc ggt tcg aac tgg aca act cct gat     1248
Gly Ser Leu Leu Asn Phe Arg Val Gly Ser Asn Trp Thr Thr Pro Asp
                405             410                 415
cgt aac ttt acc gtc gag gaa ggt gtg tcc tat ttg ctt aac aca acg     1296
Arg Asn Phe Thr Val Glu Glu Gly Val Ser Tyr Leu Leu Asn Thr Thr
            420             425                 430
gag gac tgg tat caa gac cag atc aag ggc agt tat tct cgg ggc att     1344
Glu Asp Trp Tyr Gln Asp Gln Ile Lys Gly Ser Tyr Ser Arg Gly Ile
            435             440                 445
gct cat tcc ata gat gag gtc gaa gcc aat gag aat gac ccc aag aag     1392
Ala His Ser Ile Asp Glu Val Glu Ala Asn Glu Asn Asp Pro Lys Lys
            450             455                 460
```

```
tgg atc aat cct ctc gag acg cga ttg cca ctt gct cct agc ctc aag       1440
Trp Ile Asn Pro Leu Glu Thr Arg Leu Pro Leu Ala Pro Ser Leu Lys
465                 470                 475                 480
atc tac tgc ttt tat ggt gtt gga aaa ccg acc gag cga ggg tac ttc       1488
Ile Tyr Cys Phe Tyr Gly Val Gly Lys Pro Thr Glu Arg Gly Tyr Phe
                485                 490                 495
tat aag cca ccg gat cag cca tca ttg acc aac ctc aac atc aca ata       1536
Tyr Lys Pro Pro Asp Gln Pro Ser Leu Thr Asn Leu Asn Ile Thr Ile
                500                 505                 510
gat acg ggc tat acc gaa gga gac gtg gat cat ggc gtt gtc atg ggc       1584
Asp Thr Gly Tyr Thr Glu Gly Asp Val Asp His Gly Val Val Met Gly
            515                 520                 525
gag gga gat ggt acc gtg aac ctc ctc agt aca ggc tac atg tgt aat       1632
Glu Gly Asp Gly Thr Val Asn Leu Leu Ser Thr Gly Tyr Met Cys Asn
        530                 535                 540
cat ggc tgg aat atg aaa cgc tac aac cca gca ggc gtc aag gtt aca       1680
His Gly Trp Asn Met Lys Arg Tyr Asn Pro Ala Gly Val Lys Val Thr
545                 550                 555                 560
gtt gtc gag atg cct cac gag ccg gac cgc ttc aat cct cga gga ggg       1728
Val Val Glu Met Pro His Glu Pro Asp Arg Phe Asn Pro Arg Gly Gly
                565                 570                 575
cct cgc acg gcc gac cac gtt gac atc ttg ggg cga tac aac ctg aac       1776
Pro Arg Thr Ala Asp His Val Asp Ile Leu Gly Arg Tyr Asn Leu Asn
                580                 585                 590
gag ttg ctg tta cga gta gcg agc ggc aaa ggt gac acg att acg aac       1824
Glu Leu Leu Leu Arg Val Ala Ser Gly Lys Gly Asp Thr Ile Thr Asn
            595                 600                 605
tat gtt gtg agc aac atc aaa gaa tat gca tcc agg gtt aag att tac       1872
Tyr Val Val Ser Asn Ile Lys Glu Tyr Ala Ser Arg Val Lys Ile Tyr
        610                 615                 620
gat gat gag gag act tca tag                                           1893
Asp Asp Glu Glu Thr Ser
625                 630
```

<210> 37

<211> 630
<212> PRT
<213> Fusarium graminaeum

<400> 37

```
Met Gly Lys Ser Thr Leu Arg Arg Arg Asn Gly Gln Asp Ala Thr Asn
1               5                   10                  15
Asn Asp Ser Ala Asp Ala Asp Asp Thr Pro Arg Glu Glu Ser Pro Thr
            20                  25                  30
Ala Glu Pro Thr Thr His Val Arg Val Val Gln His Ala Val Pro Arg
        35                  40                  45
Thr Arg Lys Arg Arg Asn Thr Phe Val Phe Phe Leu Gly Ser Leu Phe
    50                  55                  60
Gly Ile Ile Ala Ala Gly Phe Phe Ala Ser Ser Asn Asp Leu Ile Asp
65                  70                  75                  80
Leu Pro Glu Phe Thr Asp Leu Ser Met Asp Asn Leu Met Asp Val Leu
                85                  90                  95
Pro Ala Gly Leu Ile Lys Asp Met Arg Asp Leu Val Gln Gly Glu Arg
            100                 105                 110
Asp Ile Ala Glu Ser Tyr Glu Pro Phe Ser Val Gly Glu Lys Ala Arg
```

```
                115                        120                        125
Ser Glu Gly Leu Gly Val His His Pro Met Ile Met Ile Pro Gly Val
    130                        135                        140
Ile Ser Thr Gly Leu Glu Ser Trp Gly Thr Ala Asn Ile Ser Lys Pro
145                        150                        155                        160
Tyr Phe Arg Lys Arg Leu Trp Gly Ser Trp Thr Met Met Arg Ala Leu
                165                        170                        175
Val Met Asp Lys Glu Val Trp Lys Lys His Val Met Leu Asp Lys Arg
                180                        185                        190
Thr Gly Leu Asp Pro Pro Asp Val Lys Leu Arg Ala Ala Gln Gly Phe
                195                        200                        205
Asp Ala Thr Asp Phe Phe Ile Thr Gly Tyr Trp Ile Trp Ser Lys Ile
    210                        215                        220
Phe Glu Asn Leu Ala Ser Ile Gly Tyr Asp Pro Thr Asn Ser Phe Thr
225                        230                        235                        240
Ala Ala Tyr Asp Trp Arg Leu Ser Tyr Pro Asn Leu Glu Val Arg Asp
                245                        250                        255
Arg Tyr Phe Thr Arg Leu Lys Ser His Ile Glu Ile Ala Val Ala Thr
                260                        265                        270
Glu Asp Lys Lys Val Val Leu Ala Ser His Ser Met Gly Ser Gln Val
                275                        280                        285
Leu Tyr Tyr Phe Leu His Trp Val Gln Ser Glu Arg Gly Gly Arg Gly
    290                        295                        300
Gly Pro Asp Trp Val Glu Arg His Ile Asp Ala Trp Ile Asn Ile Ser
305                        310                        315                        320
Gly Cys Met Leu Gly Ala Val Lys Asp Leu Thr Ala Val Leu Ser Gly
                325                        330                        335
Glu Met Arg Asp Thr Ala Gln Leu Asn Pro Phe Ala Ile Tyr Gly Leu
                340                        345                        350
Glu Lys Phe Leu Ser Lys Glu Glu Arg Ala Glu Ile Phe Arg Gly Met
                355                        360                        365
Pro Gly Ile Ser Ser Met Leu Pro Ile Gly Gly Asn Ser Val Trp Gly
    370                        375                        380
Asn Leu Thr Trp Ala Pro Asp Asp Leu Pro Gly Gln Asn Arg Ser Tyr
385                        390                        395                        400
Gly Ser Leu Leu Asn Phe Arg Val Gly Ser Asn Trp Thr Thr Pro Asp
                405                        410                        415
Arg Asn Phe Thr Val Glu Glu Gly Val Ser Tyr Leu Leu Asn Thr Thr
                420                        425                        430
Glu Asp Trp Tyr Gln Asp Gln Ile Lys Gly Ser Tyr Ser Arg Gly Ile
                435                        440                        445
Ala His Ser Ile Asp Glu Val Glu Ala Asn Glu Asn Asp Pro Lys Lys
    450                        455                        460
Trp Ile Asn Pro Leu Glu Thr Arg Leu Pro Leu Ala Pro Ser Leu Lys
465                        470                        475                        480
Ile Tyr Cys Phe Tyr Gly Val Gly Lys Pro Thr Glu Arg Gly Tyr Phe
                485                        490                        495
Tyr Lys Pro Pro Asp Gln Pro Ser Leu Thr Asn Leu Asn Ile Thr Ile
                500                        505                        510
Asp Thr Gly Tyr Thr Glu Gly Asp Val Asp His Gly Val Val Met Gly
                515                        520                        525
Glu Gly Asp Gly Thr Val Asn Leu Leu Ser Thr Gly Tyr Met Cys Asn
    530                        535                        540
His Gly Trp Asn Met Lys Arg Tyr Asn Pro Ala Gly Val Lys Val Thr
545                        550                        555                        560
Val Val Glu Met Pro His Glu Pro Asp Arg Phe Asn Pro Arg Gly Gly
                565                        570                        575
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Pro Arg Thr Ala Asp His Val Asp Ile Leu Gly Arg Tyr Asn Leu Asn
        580   585   590
Glu Leu Leu Leu Arg Val Ala Ser Gly Lys Gly Asp Thr Ile Thr Asn
        595   600   605
Tyr Val Val Ser Asn Ile Lys Glu Tyr Ala Ser Arg Val Lys Ile Tyr
        610   615   620
Asp Asp Glu Glu Thr Ser
625   630

<210> 38

<211> 849
<212> DNA
<213> Caenorhabditis elegans

<220>
<221> CDS
<222> (1)..(849)
<223> Acyl-CoA:lysophospholipid acyltransferase

<400> 38

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atg gag aac ttc tgg tcg atc gtc gtg ttt ttt cta ctc tca att ctc      48
Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu
1               5                   10                  15
ttc att tta tat aac ata tcg aca gta tgc cac tac tat atg cgg att      96
Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Met Arg Ile
            20                  25                  30
tcg ttt tat tac ttc aca att tta ttg cat gga atg gaa gtt tgt gtt     144
Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
            35                  40                  45
aca atg atc cct tct tgg cta aat ggg aag ggt gct gat tac gtg ttt     192
Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
        50                  55                  60
cac tcg ttt ttc tat tgg tgt aaa tgg act ggt gtt cat aca aca gtc     240
His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val
65                  70                  75                  80
tat gga tat gaa aaa aca caa gtt gaa ggt ccg gct gta gtt att tgt     288
Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys
                85                  90                  95
aat cat cag agt tct ctc gac att cta tcg atg gca tca atc tgg ccg     336
Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro
            100                 105                 110
aag aat tgt gtt gta atg atg aaa cga att ctt gcc tat gtt cca ttc     384
Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe
            115                 120                 125
ttc aat ctc gga gcc tac ttt tcc aac aca atc ttc atc gat cga tat     432
Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr
        130                 135                 140
aac cgt gaa cgt gcg atg gct tca gtt gat tat tgt gca tct gaa atg     480
Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met
145                 150                 155                 160
aag aac aga aat ctt aaa ctt tgg gta ttt ccg gaa gga aca aga aat     528
Lys Asn Arg Asn Leu Lys Leu Trp Val Phe Pro Glu Gly Thr Arg Asn
            165                 170                 175
cgt gaa gga ggg ttc att cca ttc aag aaa gga gca ttc aat att gca     576
Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala
```

```
               180                      185                      190
gtt cgt gcg cag att ccc att att cca gtt gta .ttc tca gac tat cgg      624
Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg
         195                      200                      205
gat ttc tac tca aag cca ggc cga tat ttc aag aat gat gga gaa gtt      672
Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val
         210                      215                      220
gtt att cga gtt ctg gat gcg att cca aca aaa ggg ctc act ctt gat      720
Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp
225                      230                      235                      240
gac gtc agc gag ttg tct gat atg tgt cgg gac gtt atg ttg gca gcc      768
Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala
                   245                      250                      255
tat aag gaa gtt act cta gaa gct cag caa cga aat gcg aca cgg cgt      816
Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg
                   260                      265                      270
gga gaa aca aaa gac ggg aag aaa tct gag taa                          849
Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu
              275                      280


<210>   39

<211>   282
<212>   PRT
<213>   Caenorhabditis elegans

<400>   39

Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu
1                 5                     10                      15
Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Met Arg Ile
              20                      25                      30
Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
              35                      40                      45
Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
      50                      55                      60
His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val
65                      70                      75                      80
Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys
                   85                      90                      95
Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro
              100                     105                     110
Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe
              115                     120                     125
Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr
              130                     135                     140
Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met
145                     150                     155                     160
Lys Asn Arg Asn Leu Lys Leu Trp Val Phe Pro Glu Gly Thr Arg Asn
                   165                     170                     175
Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala
              180                     185                     190
Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg
         195                     200                     205
Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val
         210                     215                     220
Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp
```

```
          225                     230                     235                     240
          Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala
                          245                     250                     255
          Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg
                          260                     265                     270
          Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu
                  275                     280
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<210> 40

<211> 849
<212> DNA
<213> Caenorhabditis elegans

<220>
<221> CDS
<222> (1)..(849)
<223> Acyl-CoA:lysophospholipid acyltransferase

<400> 40

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atg gag aac ttc tgg tcg atc gtc gtg ttt ttt cta ctc tca att ctc        48
Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu
1               5                       10                      15
ttc att tta tat aac ata tcg aca gta tgc cac tac tat atg cgg att        96
Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Met Arg Ile
                20                      25                      30
tcg ttt tat tac ttc aca att tta ttg cat gga atg gaa gtt tgt gtt       144
Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
            35                      40                      45
aca atg atc cct tct tgg cta aat ggg aag ggt gct gat tac gtg ttt       192
Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
        50                      55                      60
cac tcg ttt ttc tat tgg tgt aaa tgg act ggt gtt cat aca aca gtc       240
His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val
65                      70                      75                      80
tat gga tat gaa aaa aca caa gtt gaa ggt ccg gct gta gtt att tgt       288
Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys
                85                      90                      95
aat cat cag agt tct ctc gac att cta tcg atg gca tca atc tgg ccg       336
Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro
                100                     105                     110
aag aat tgt gtt gta atg atg aaa cga att ctt gcc tat gtt cca ttc       384
Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe
            115                     120                     125
ttc aat ctc gga gcc tac ttt tcc aac aca atc ttc atc gat cga tat       432
Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr
        130                     135                     140
aac cgt gaa cgt gcg atg gct tca gtt gat tat tgt gca tct gaa atg       480
Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met
145                     150                     155                     160
aag aac aga aat ctt aaa ctt tgg gta tct ccg gaa gga aca aga aat       528
Lys Asn Arg Asn Leu Lys Leu Trp Val Ser Pro Glu Gly Thr Arg Asn
                165                     170                     175
cgt gaa gga ggg ttc att cca ttc aag aaa gga gca ttc aat att gca       576
Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala
                180                     185                     190
gtt cgt gcg cag att ccc att att cca gtt gta ttc tca gac tat cgg       624
```

```
Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg
        195               200               205
gat ttc tac tca aag cca ggc cga tat ttc aag aat gat gga gaa gtt    672
Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val
        210               215               220
gtt att cga gtt ctg gat gcg att cca aca aaa ggg ctc act ctt gat    720
Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp
225               230               235               240
gac gtc agc gag ttg tct gat atg tgt cgg gac gtt atg ttg gca gcc    768
Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala
                245               250               255
tat aag gaa gtt act cta gaa gct cag caa cga aat gcg aca cgg cgt    816
Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg
                260               265               270
gga gaa aca aaa gac ggg aag aaa tct gag taa                        849
Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu
                275               280
```

<210> 41

<211> 282
<212> PRT
<213> Caenorhabditis elegans

<400> 41

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Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu
1               5                   10                  15
Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Met Arg Ile
            20                  25                  30
Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
            35                  40                  45
Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
        50                  55                  60
His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val
65                  70                  75                  80
Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys
                85                  90                  95
Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro
            100                 105                 110
Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe
            115                 120                 125
Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr
        130                 135                 140
Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met
145                 150                 155                 160
Lys Asn Arg Asn Leu Lys Leu Trp Val Ser Pro Glu Gly Thr Arg Asn
                165                 170                 175
Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala
            180                 185                 190
Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg
            195                 200                 205
Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val
        210                 215                 220
Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp
225                 230                 235                 240
Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala
```

```
                      245                    250                    255
Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg
                260                    265                    270
Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu
          275                    280


<210>  42

<211>  849
<212>  DNA
<213>  Caenorhabditis elegans

<220>
<221>  CDS
<222>  (1)..(849)
<223>  Acyl-CoA:lysophospholipid acyltransferase

<400>  42

atg gag aac ttc tgg tcg atc gtc gtg ttt ttt cta ctc tca att ctc        48
Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu
1               5                   10                  15
ttc att tta tat aac ata tcg aca gta tgc cac tac tat gtg cgg att        96
Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Val Arg Ile
            20                  25                  30
tcg ttt tat tac ttc aca att tta ttg cat gga atg gaa gtt tgt gtt       144
Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
        35                  40                  45
aca atg atc cct tct tgg cta aat ggg aag ggt gct gat tac gtg ttt       192
Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
    50                  55                  60
cac tcg ttt ttc tat tgg tgt aaa tgg act ggt gtt cat aca aca gtc       240
His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val
65                  70                  75                  80
tat gga tat gaa aaa aca caa gtt gaa ggt ccg gct gta gtt att tgt       288
Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys
                85                  90                  95
aat cat cag agt tct ctc gac att cta tcg atg gca tca atc tgg ccg       336
Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro
            100                 105                 110
aag aat tgt gtt gta atg atg aaa cga att ctt gcc tat gtt cca ttc       384
Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe
        115                 120                 125
ttc aat ctc gga gcc tac ttt tcc aac aca atc ttc atc gat cga tat       432
Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr
    130                 135                 140
aac cgt gaa cgt gcg atg gct tca gtt gat tat tgt gca tct gaa atg       480
Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met
145                 150                 155                 160
aag aac aga aat ctt aaa ctt tgg gta ttt ccg gaa gga aca aga aat       528
Lys Asn Arg Asn Leu Lys Leu Trp Val Phe Pro Glu Gly Thr Arg Asn
                165                 170                 175
cgt gaa gga ggg ttc att cca ttc aag aaa gga gca ttc aat att gca       576
Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala
            180                 185                 190
gtt cgt gcg cag att ccc att att cca gtt gta ttc tca gac tat cgg       624
Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg
```

```
                195                       200                       205
gat ttc tac tca aag cca ggc cga tat ttc aag aat gat gga gaa gtt       672
Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val
    210                       215                       220
gtt att cga gtt ctg gat gcg att cca aca aaa ggg ctc act ctt gat       720
Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp
225                       230                       235                       240
gac gtc agc gag ttg tct gat atg tgt cgg gac gtt atg ttg gca gcc       768
Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala
                245                       250                       255
tat aag gaa gtt act cta gaa gct cag caa cga aat gcg aca cgg cgt       816
Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg
                260                       265                       270
gga gaa aca aaa gac ggg aag aaa tct gag taa                           849
Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu
                275                       280
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<210> 43

<211> 282
<212> PRT
<213> Caenorhabditis elegans

<400> 43

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Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu
1               5                       10                      15
Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Val Arg Ile
            20                      25                      30
Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
            35                      40                      45
Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
        50                      55                      60
His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val
65                      70                      75                      80
Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys
                85                      90                      95
Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro
            100                     105                     110
Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe
            115                     120                     125
Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr
            130                     135                     140
Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met
145                     150                     155                     160
Lys Asn Arg Asn Leu Lys Leu Trp Val Phe Pro Glu Gly Thr Arg Asn
                165                     170                     175
Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala
            180                     185                     190
Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg
            195                     200                     205
Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val
            210                     215                     220
Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp
225                     230                     235                     240
Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala
                245                     250                     255
```

```
Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg
            260                 265                 270
Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu
        275                 280
```

<210> 44

<211> 849
<212> DNA
<213> Caenorhabditis elegans

<220>
<221> CDS
<222> (1)..(849)
<223> Acyl-CoA:lysophospholipid acyltransferase

<400> 44

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atg gag aac ttc tgg tcg atc gtc gtg ttt ttt cta ctc tca att ctc     48
Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu
1               5                   10                  15
ttc att tta tat aac ata tcg aca gta tgc cac tac tat atg cgg att     96
Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Met Arg Ile
            20                  25                  30
tcg ttt tat tac ttc aca att tta ttg cat gga atg gaa gtt tgt gtt    144
Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
        35                  40                  45
aca atg atc cct tct tgg cta aat ggg aag ggt gct gat tac gtg ttt    192
Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
    50                  55                  60
cac tcg ttt ttc tat tgg tgt aaa tgg act ggt gtt cat aca aca gtc    240
His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val
65                  70                  75                  80
tat gga tat gaa aaa aca caa gtt gaa ggt ccg gcc gta gtt att tgt    288
Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys
                85                  90                  95
aat cat cag ggt tct ctc gac att cta tcg atg gca tca atc tgg ccg    336
Asn His Gln Gly Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro
            100                 105                 110
aag aat tgt gtt gta atg atg aaa cga att ctt gcc tat gtt cca ttc    384
Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe
        115                 120                 125
ttc aat ctc gga gcc tac ttt tcc aac aca atc ttc atc gat cga tat    432
Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr
    130                 135                 140
aac cgt gaa cgt gcg atg gct tca gtt gat tat tgt gca tct gaa atg    480
Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met
145                 150                 155                 160
aag aac aga aat ctt aaa ctt tgg gta ttt ccg gaa gga aca aga aat    528
Lys Asn Arg Asn Leu Lys Leu Trp Val Phe Pro Glu Gly Thr Arg Asn
                165                 170                 175
cgt gaa gga ggg ttc att cca ttc aag aaa gga gca ttc aat att gca    576
Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala
            180                 185                 190
gtt cgt gcg cag att ccc att att cca gtt gta ttc tca gac tat cgg    624
Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg
```

```
                195                     200                     205
gat ttc tac tca aag cca ggc cga tat ttc aag aat gat gga gaa gtt        672
Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val
    210                     215                     220
gtt att cga gtt ctg gat gcg att cca aca aaa ggg ctc act ctt gat        720
Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp
225                     230                     235                 240
gac gtc agc gag ttg tct gat atg tgt cgg gac gtt atg ttg gca gcc        768
Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala
                245                     250                     255
tat aag gaa gtt act cta gaa gct cag caa cga aat gcg aca cgg cgt        816
Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg
                260                     265                     270
gga gaa aca aaa gac ggg aag aaa tct gag taa                            849
Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu
                275                     280


<210>  45

<211>  282
<212>  PRT
<213>  Caenorhabditis elegans

<400>  45


Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu
1               5                   10                  15
Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Met Arg Ile
            20                  25                  30
Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
            35                  40                  45
Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
        50                  55                  60
His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val
65                  70                  75                  80
Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys
                85                  90                  95
Asn His Gln Gly Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro
            100                 105                 110
Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe
        115                 120                 125
Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr
        130                 135                 140
Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met
145                 150                 155                 160
Lys Asn Arg Asn Leu Lys Leu Trp Val Phe Pro Glu Gly Thr Arg Asn
                165                 170                 175
Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala
            180                 185                 190
Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg
            195                 200                 205
Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val
    210                     215                 220
Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp
225                     230                     235                 240
Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala
                245                     250                     255
```

```
Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg
        260                 265             270
Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu
        275             280


<210>  46

<211>  1578
<212>  DNA
<213>  Physcomitrella patens

<220>
<221>  CDS
<222>  (1)..(1578)
<223>  Delta-6-desaturase


<400>  46

atg gta ttc gcg ggc ggt gga ctt cag cag ggc tct ctc gaa gaa aac        48
Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn
1               5                   10                  15
atc gac gtc gag cac att gcc agt atg tct ctc ttc agc gac ttc ttc        96
Ile Asp Val Glu His Ile Ala Ser Met Ser Leu Phe Ser Asp Phe Phe
            20                  25                  30
agt tat gtg tct tca act gtt ggt tcg tgg agc gta cac agt ata caa       144
Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln
        35                  40                  45
cct ttg aag cgc ctg acg agt aag aag cgt gtt tcg gaa agc gct gcc       192
Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala
    50                  55                  60
gtg caa tgt ata tca gct gaa gtt cag aga aat tcg agt acc cag gga       240
Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly
65                  70                  75                  80
act gcg gag gca ctc gca gaa tca gtc gtg aag ccc acg aga cga agg       288
Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg
                85                  90                  95
tca tct cag tgg aag aag tcg aca cac ccc cta tca gaa gta gca gta       336
Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val
            100                 105                 110
cac aac aag cca agc gat tgc tgg att gtt gta aaa aac aag gtg tat       384
His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr
        115                 120                 125
gat gtt tcc aat ttt gcg gac gag cat ccc gga gga tca gtt att agt       432
Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser
        130                 135                 140
act tat ttt gga cga gac ggc aca gat gtt ttc tct agt ttt cat gca       480
Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala
145                 150                 155                 160
gct tct aca tgg aaa att ctt caa gac ttt tac att ggt gac gtg gag       528
Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu
            165                 170                 175
agg gtg gag ccg act cca gag ctg ctg aaa gat ttc cga gaa atg aga       576
Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg
            180                 185                 190
gct ctt ttc ctg agg gag caa ctt ttc aaa agt tcg aaa ttg tac tat       624
Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr
        195                 200                 205
```

```
gtt atg aag ctg ctc acg aat gtt gct att ttt gct gcg agc att gca        672
Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala
    210                 215                 220

ata ata tgt tgg agc aag act att tca gcg gtt ttg gct tca gct tgt        720
Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys
225                 230                 235                 240

atg atg gct ctg tgt ttc caa cag tgc gga tgg cta tcc cat gat ttt        768
Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe
                245                 250                 255

ctc cac aat cag gtg ttt gag aca cgc tgg ctt aat gaa gtt gtc ggg        816
Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly
                260                 265                 270

tat gtg atc ggc aac gcc gtt ctg ggg ttt agt aca ggg tgg tgg aag        864
Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys
                275                 280                 285

gag aag cat aac ctt cat cat gct gct cca aat gaa tgc gat cag act        912
Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr
    290                 295                 300

tac caa cca att gat gaa gat att gat act ctc ccc ctc att gcc tgg        960
Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp
305                 310                 315                 320

agc aag gac ata ctg gcc aca gtt gag aat aag aca ttc ttg cga atc       1008
Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile
                325                 330                 335

ctc caa tac cag cat ctg ttc ttc atg ggt ctg tta ttt ttc gcc cgt       1056
Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg
                340                 345                 350

ggt agt tgg ctc ttt tgg agc tgg aga tat acc tct aca gca gtg ctc       1104
Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu
                355                 360                 365

tca cct gtc gac agg ttg ttg gag aag gga act gtt ctg ttt cac tac       1152
Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr
    370                 375                 380

ttt tgg ttc gtc ggg aca gcg tgc tat ctt ctc cct ggt tgg aag cca       1200
Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro
385                 390                 395                 400

tta gta tgg atg gcg gtg act gag ctc atg tcc ggc atg ctg ctg ggc       1248
Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly
                405                 410                 415

ttt gta ttt gta ctt agc cac aat ggg atg gag gtt tat aat tcg tct       1296
Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser
                420                 425                 430

aaa gaa ttc gtg agt gca cag atc gta tcc aca cgg gat atc aaa gga       1344
Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly
                435                 440                 445

aac ata ttc aac gac tgg ttc act ggt ggc ctt aac agg caa ata gag       1392
Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu
    450                 455                 460

cat cat ctt ttc cca aca atg ccc agg cat aat tta aac aaa ata gca       1440
His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala
465                 470                 475                 480

cct aga gtg gag gtg ttc tgt aag aaa cac ggt ctg gtg tac gaa gac       1488
Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp
                485                 490                 495

gta tct att gct acc ggc act tgc aag gtt ttg aaa gca ttg aag gaa       1536
Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu
                500                 505                 510
```

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gtc gcg gag gct gcg gca gag cag cat gct acc acc agt taa            1578
Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser
        515                 520                 525
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<210> 47

<211> 525
<212> PRT
<213> Physcomitrella patens

<400> 47

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Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn
1               5                   10                  15
Ile Asp Val Glu His Ile Ala Ser Met Ser Leu Phe Ser Asp Phe Phe
        20                  25                  30
Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln
        35                  40                  45
Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala
    50                  55                  60
Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly
65                  70                  75                  80
Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg
                85                  90                  95
Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val
            100                 105                 110
His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr
        115                 120                 125
Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser
        130                 135                 140
Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala
145                 150                 155                 160
Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu
                165                 170                 175
Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg
                180                 185                 190
Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr
            195                 200                 205
Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala
    210                 215                 220
Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys
225                 230                 235                 240
Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe
                245                 250                 255
Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly
            260                 265                 270
Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys
        275                 280                 285
Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr
    290                 295                 300
Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp
305                 310                 315                 320
Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile
                325                 330                 335
Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg
            340                 345                 350
Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu
```

```
                   355                        360                        365
Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr
        370                        375                        380
Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro
385                        390                        395                        400
Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly
                   405                        410                        415
Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser
                   420                        425                        430
Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly
                   435                        440                        445
Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu
                   450                        455                        460
His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala
465                        470                        475                        480
Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp
                   485                        490                        495
Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu
                   500                        505                        510
Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser
                   515                        520                        525
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<210> 48

<211> 1192
<212> DNA
<213> Physcomitrella patens

<220>
<221> CDS
<222> (58)..(930)
<223> Delta-6-elongase

<400> 48

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ctgcttcgtc tcatcttggg ggtgtgattc gggagtgggt tgagttggtg gagcgca              57
atg gag gtc gtg gag aga ttc tac ggt gag ttg gat ggg aag gtc tcg            105
Met Glu Val Val Glu Arg Phe Tyr Gly Glu Leu Asp Gly Lys Val Ser
1               5                   10                  15
cag ggc gtg aat gca ttg ctg ggt agt ttt ggg gtg gag ttg acg gat            153
Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr Asp
            20                  25                  30
acg ccc act acc aaa ggc ttg ccc ctc gtt gac agt ccc aca ccc atc            201
Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile
            35                  40                  45
gtc ctc ggt gtt tct gta tac ttg act att gtc att gga ggg ctt ttg           249
Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu
        50                  55                  60
tgg ata aag gcc agg gat ctg aaa ccg cgc gcc tcg gag cca ttt ttg           297
Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu
65                  70                  75                  80
ctc caa gct ttg gtg ctt gtg cac aac ctg ttc tgt ttt gcg ctc agt          345
Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser
            85                  90                  95
ctg tat atg tgc gtg ggc atc gct tat cag gct att acc tgg cgg tac          393
Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr
            100                 105                 110
```

```
tct ctc tgg ggc aat gca tac aat cct aaa cat aaa gag atg gcg att    441
Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile
        115                 120                 125
ctg gta tac ttg ttc tac atg tct aag tac gtg gaa ttc atg gat acc    489
Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr
        130                 135                 140
gtt atc atg ata ctg aag cgc agc acc agg caa ata agc ttc ctc cac    537
Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His
145                 150                 155                 160
gtt tat cat cat tct tca att tcc ctc att tgg tgg gct att gct cat    585
Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His
                165                 170                 175
cac gct cct ggc ggt gaa gca tat tgg tct gcg gct ctg aac tca gga    633
His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly
            180                 185                 190
gtg cat gtt ctc atg tat gcg tat tac ttc ttg gct gcc tgc ctt cga    681
Val His Val Leu Met Tyr Ala Tyr Tyr Phe Leu Ala Ala Cys Leu Arg
            195                 200                 205
agt agc cca aag tta aaa aat aag tac ctt ttt tgg ggc agg tac ttg    729
Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr Leu
        210                 215                 220
aca caa ttc caa atg ttc cag ttt atg ctg aac tta gtg cag gct tac    777
Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala Tyr
225                 230                 235                 240
tac gac atg aaa acg aat gcg cca tat cca caa tgg ctg atc aag att    825
Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile
                245                 250                 255
ttg ttc tac tac atg atc tcg ttg ctg ttt ctt ttc ggc aat ttt tac    873
Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr
        260                 265                 270
gta caa aaa tac atc aaa ccc tct gac gga aag caa aag gga gct aaa    921
Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala Lys
        275                 280                 285
act gag tga gctgtatcaa gccatagaaa ctctattatg ttagaacctg           970
Thr Glu
290
aagttggtgc tttcttatct ccacttatct tttaagcagc atcagttttg aaatgatgtg  1030
tgggcgtggt ctgcaagtag tcatcaatat aatcggcctg agcacttcag atggattgtt  1090
agaacatgag taaaagcggt tattacggtg tttattttgt accaaatcac cgcacgggtg  1150
aattgaaata tttcagattt gatcaatttc atctgaaaaa aa                     1192
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<210> 49

<211> 290
<212> PRT
<213> Physcomitrella patens

<400> 49

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Met Glu Val Val Glu Arg Phe Tyr Gly Glu Leu Asp Gly Lys Val Ser
1               5                   10                  15
Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr Asp
        20                  25                  30
Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile
        35                  40                  45
Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu
    50                  55                  60
```

```
Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu
65                  70                  75                  80
Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser
                85                  90                  95
Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr
            100                 105                 110
Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile
        115                 120                 125
Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr
    130                 135                 140
Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His
145                 150                 155                 160
Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His
                165                 170                 175
His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly
            180                 185                 190
Val His Val Leu Met Tyr Ala Tyr Tyr Phe Leu Ala Ala Cys Leu Arg
            195                 200                 205
Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr Leu
        210                 215                 220
Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala Tyr
225                 230                 235                 240
Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile
            .   245                 250                 255
Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr
            260                 265                 270
Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala Lys
        275                 280                 285
Thr Glu
    290


<210>  50

<211>  1410
<212>  DNA
<213>  Phaeodactylum tricornutum

<220>
<221>  CDS
<222>  (1)..(1410)
<223>  Delta-5-desaturase

<400>  50

atg gct ccg gat gcg gat aag ctt cga caa cgc cag acg act gcg gta      48
Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val
1               5                   10                  15
gcg aag cac aat gct gct acc ata tcg acg cag gaa cgc ctt tgc agt      96
Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser
            20                  25                  30
ctg tct tcg ctc aaa ggc gaa gaa gtc tgc atc gac gga atc atc tat     144
Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr
        35                  40                  45
gac ctc caa tca ttc gat cat ccc ggg ggt gaa acg atc aaa atg ttt     192
Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe
    50                  55                  60
ggt ggc aac gat gtc act gta cag tac aag atg att cac ccg tac cat     240
```

```
Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His
65                  70                  75                  80
acc gag aag cat ttg gaa aag atg aag cgt gtc ggc aag gtg acg gat      288
Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp
                85                  90                  95
ttc gtc tgc gag tac aag ttc gat acc gaa ttt gaa cgc gaa atc aaa      336
Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys
                100                 105                 110
cga gaa gtc ttc aag att gtg cga cga ggc aag gat ttc ggt act ttg      384
Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu
            115                 120                 125
gga tgg ttc ttc cgt gcg ttt tgc tac att gcc att ttc ttc tac ctg      432
Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu
        130                 135                 140
cag tac cat tgg gtc acc acg gga acc tct tgg ctg ctg gcc gtg gcc      480
Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala
145                 150                 155                 160
tac gga atc tcc caa gcg atg att ggc atg aat gtc cag cac gat gcc      528
Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala
                165                 170                 175
aac cac ggg gcc acc tcc aag cgt ccc tgg gtc aac gac atg cta ggc      576
Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly
            180                 185                 190
ctc ggt gcg gat ttt att ggt ggt tcc aag tgg ctc tgg cag gaa caa      624
Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln
            195                 200                 205
cac tgg acc cac cac gct tac acc aat cac gcc gag atg gat ccc gat      672
His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp
        210                 215                 220
agc ttt ggt gcc gaa cca atg ctc cta ttc aac gac tat ccc ttg gat      720
Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp
225                 230                 235                 240
cat ccc gct cgt acc tgg cta cat cgc ttt caa gca ttc ttt tac atg      768
His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met
                245                 250                 255
ccc gtc ttg gct gga tac tgg ttg tcc gct gtc ttc aat cca caa att      816
Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile
            260                 265                 270
ctt gac ctc cag caa cgc ggc gca ctt tcc gtc ggt atc cgt ctc gac      864
Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp
            275                 280                 285
aac gct ttc att cac tcg cga cgc aag tat gcg gtt ttc tgg cgg gct      912
Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala
        290                 295                 300
gtg tac att gcg gtg aac gtg att gct ccg ttt tac aca aac tcc ggc      960
Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly
305                 310                 315                 320
ctc gaa tgg tcc tgg cgt gtc ttt gga aac atc atg ctc atg ggt gtg      1008
Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val
                325                 330                 335
gcg gaa tcg ctc gcg ctg gcg gtc ctg ttt tcg ttg tcg cac aat ttc      1056
Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe
            340                 345                 350
gaa tcc gcg gat cgc gat ccg acc gcc cca ctg aaa aag acg gga gaa      1104
Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu
            355                 360                 365
cca gtc gac tgg ttc aag aca cag gtc gaa act tcc tgc act tac ggt      1152
```

```
Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly
    370                 375             380
gga ttc ctt tcc ggt tgc ttc acg gga ggt ctc aac ttt cag gtt gaa      1200
Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu
385                 390             395                 400
cac cac ttg ttc cca cgc atg agc agc gct tgg tat ccc tac att gcc      1248
His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala
                405             410                 415
ccc aag gtc cgc gaa att tgc gcc aaa cac ggc gtc cac tac gcc tac      1296
Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr
                420             425                 430
tac ccg tgg atc cac caa aac ttt ctc tcc acc gtc cgc tac atg cac      1344
Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His
            435                 440                 445
gcg gcc ggg acc ggt gcc aac tgg cgc cag atg gcc aga gaa aat ccc      1392
Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro
    450                 455             460
ttg acc gga cgg gcg taa                                               1410
Leu Thr Gly Arg Ala
465
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<210> 51

<211> 469
<212> PRT
<213> Phaeodactylum tricornutum

<400> 51

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Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val
1               5                   10              15
Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser
            20              25              30
Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr
        35              40              45
Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe
    50              55              60
Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His
65              70              75                  80
Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp
            85              90                  95
Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys
            100             105             110
Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu
        115             120             125
Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu
    130             135             140
Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala
145             150             155                 160
Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala
            165             170                 175
Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly
            180             185             190
Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln
        195             200             205
His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp
    210             215             220
```

Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp
225   230   235   240
His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met
                245   250   255
Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile
            260   265   270
Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp
        275   280   285
Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala
    290   295   300
Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly
305   310   315   320
Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val
            325   330   335
Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe
            340   345   350
Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu
            355   360   365
Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly
            370   375   380
Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu
385   390   395   400
His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala
            405   410   415
Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr
            420   425   430
Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His
            435   440   445
Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro
450   455   460
Leu Thr Gly Arg Ala
465

<210> 52

<211> 3598
<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
<223> Sequence represents a plant promoter-terminator expression cassette
      in vector pUC19

<400> 52

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<212>   DNA
<213>   artificial sequence

<220>
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<223>  Sequence represents a plant promoter-terminator expression cassette
       in vector pUC19

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<211>  3584
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<213>  artificial sequence

<220>
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<223>  Sequence represents a plant promoter-terminator expression cassette
       in vector pUC19

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<213> artificial sequence

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<223> Sequence represents a plant promoter-terminator expression cassette
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Leu Asp Gly Lys Val Ser Gln Gly Val Asn Ala Leu Leu Gly Ser Phe
            15                  20                  25
ggg gtg gag ttg acg gat acg ccc act acc aaa ggc ttg ccc ctc gtt  11668
Gly Val Glu Leu Thr Asp Thr Pro Thr Thr Lys Gly Leu Pro Leu Val
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gac agt ccc aca ccc atc gtc ctc ggt gtt tct gta tac ttg act att  11716
```

```
Asp Ser Pro Thr Pro Ile Val Leu Gly Val Ser Val Tyr Leu Thr Ile
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gtc att gga ggg ctt ttg tgg ata aag gcc agg gat ctg aaa ccg cgc    11764
Val Ile Gly Gly Leu Leu Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg
        60                      65                      70
gcc tcg gag cca ttt ttg ctc caa gct ttg gtg ctt gtg cac aac ctg    11812
Ala Ser Glu Pro Phe Leu Leu Gln Ala Leu Val Leu Val His Asn Leu
75                      80                      85              90
ttc tgt ttt gcg ctc agt ctg tat atg tgc gtg ggc atc gct tat cag    11860
Phe Cys Phe Ala Leu Ser Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln
                    95                      100                 105
gct att acc tgg cgg tac tct ctc tgg ggc aat gca tac aat cct aaa    11908
Ala Ile Thr Trp Arg Tyr Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys
            110                     115                     120
cat aaa gag atg gcg att ctg gta tac ttg ttc tac atg tct aag tac    11956
His Lys Glu Met Ala Ile Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr
            125                     130                     135
gtg gaa ttc atg gat acc gtt atc atg ata ctg aag cgc agc acc agg    12004
Val Glu Phe Met Asp Thr Val Ile Met Ile Leu Lys Arg Ser Thr Arg
        140                     145                     150
caa ata agc ttc ctc cac gtt tat cat cat tct tca att tcc ctc att    12052
Gln Ile Ser Phe Leu His Val Tyr His His Ser Ser Ile Ser Leu Ile
155                     160                     165             170
tgg tgg gct att gct cat cac gct cct ggc ggt gaa gca tat tgg tct    12100
Trp Trp Ala Ile Ala His His Ala Pro Gly Gly Glu Ala Tyr Trp Ser
                    175                     180                 185
gcg gct ctg aac tca gga gtg cat gtt ctc atg tat gcg tat tac ttc    12148
Ala Ala Leu Asn Ser Gly Val His Val Leu Met Tyr Ala Tyr Tyr Phe
            190                     195                     200
ttg gct gcc tgc ctt cga agt agc cca aag tta aaa aat aag tac ctt    12196
Leu Ala Ala Cys Leu Arg Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu
            205                     210                     215
ttt tgg ggc agg tac ttg aca caa ttc caa atg ttc cag ttt atg ctg    12244
Phe Trp Gly Arg Tyr Leu Thr Gln Phe Gln Met Phe Gln Phe Met Leu
        220                     225                     230
aac tta gtg cag gct tac tac gac atg aaa acg aat gcg cca tat cca    12292
Asn Leu Val Gln Ala Tyr Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro
235                     240                     245                 250
caa tgg ctg atc aag att ttg ttc tac tac atg atc tcg ttg ctg ttt    12340
Gln Trp Leu Ile Lys Ile Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe
                    255                     260                 265
ctt ttc ggc aat ttt tac gta caa aaa tac atc aaa ccc tct gac gga    12388
Leu Phe Gly Asn Phe Tyr Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly
            270                     275                     280
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Lys Gln Lys Gly Ala Lys Thr Glu
            285                     290
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```

```
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tgacatccac ttggaggatg caataatgaa gaaaactaca aatttacatg caactagtta    13215
tgcatgtagt ctatataatg aggattttgc aatactttca ttcatacaca ctcactaagt    13275
tttacacgat tataatttct tcatagccag cggatcc atg gta ttc gcg ggc ggt    13330
                                          Met Val Phe Ala Gly Gly
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gga ctt cag cag ggc tct ctc gaa gaa aac atc gac gtc gag cac att    13378
Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn Ile Asp Val Glu His Ile
            300                 305                 310
```

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gcc agt atg tct ctc ttc agc gac ttc ttc agt tat gtg tct tca act    13426
Ala Ser Met Ser Leu Phe Ser Asp Phe Phe Ser Tyr Val Ser Ser Thr
            315                 320                 325
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```
gtt ggt tcg tgg agc gta cac agt ata caa cct ttg aag cgc ctg acg    13474
Val Gly Ser Trp Ser Val His Ser Ile Gln Pro Leu Lys Arg Leu Thr
    330                 335                 340
```

```
agt aag aag cgt gtt tcg gaa agc gct gcc gtg caa tgt ata tca gct    13522
Ser Lys Lys Arg Val Ser Glu Ser Ala Ala Val Gln Cys Ile Ser Ala
345             350                 355                 360
```

```
gaa gtt cag aga aat tcg agt acc cag gga act gcg gag gca ctc gca    13570
Glu Val Gln Arg Asn Ser Ser Thr Gln Gly Thr Ala Glu Ala Leu Ala
                365                 370                 375
```

```
gaa tca gtc gtg aag ccc acg aga cga agg tca tct cag tgg aag aag    13618
Glu Ser Val Val Lys Pro Thr Arg Arg Arg Ser Ser Gln Trp Lys Lys
            380                 385                 390
```

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tcg aca cac ccc cta tca gaa gta gca gta cac aac aag cca agc gat    13666
Ser Thr His Pro Leu Ser Glu Val Ala Val His Asn Lys Pro Ser Asp
            395                 400                 405
```

```
tgc tgg att gtt gta aaa aac aag gtg tat gat gtt tcc aat ttt gcg    13714
Cys Trp Ile Val Val Lys Asn Lys Val Tyr Asp Val Ser Asn Phe Ala
    410                 415                 420
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gac gag cat ccc gga gga tca gtt att agt act tat ttt gga cga gac    13762
Asp Glu His Pro Gly Gly Ser Val Ile Ser Thr Tyr Phe Gly Arg Asp
425             430                 435                 440
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ggc aca gat gtt ttc tct agt ttt cat gca gct tct aca tgg aaa att    13810
Gly Thr Asp Val Phe Ser Ser Phe His Ala Ala Ser Thr Trp Lys Ile
                445                 450                 455
```

```
ctt caa gac ttt tac att ggt gac gtg gag agg gtg gag ccg act cca    13858
Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu Arg Val Glu Pro Thr Pro
            460                 465                 470
```

```
gag ctg ctg aaa gat ttc cga gaa atg aga gct ctt ttc ctg agg gag    13906
Glu Leu Leu Lys Asp Phe Arg Glu Met Arg Ala Leu Phe Leu Arg Glu
            475                 480                 485
```

```
caa ctt ttc aaa agt tcg aaa ttg tac tat gtt atg aag ctg ctc acg    13954
Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr Val Met Lys Leu Leu Thr
            490                 495                 500
```

```
aat gtt gct att ttt gct gcg agc att gca ata ata tgt tgg agc aag    14002
Asn Val Ala Ile Phe Ala Ala Ser Ile Ala Ile Ile Cys Trp Ser Lys
505             510                 515                 520
```

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act att tca gcg gtt ttg gct tca gct tgt atg atg gct ctg tgt ttc    14050
Thr Ile Ser Ala Val Leu Ala Ser Ala Cys Met Met Ala Leu Cys Phe
                525                 530                 535
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caa cag tgc gga tgg cta tcc cat gat ttt ctc cac aat cag gtg ttt    14098
Gln Gln Cys Gly Trp Leu Ser His Asp Phe Leu His Asn Gln Val Phe
                540                 545                 550
```

```
gag aca cgc tgg ctt aat gaa gtt gtc ggg tat gtg atc ggc aac gcc    14146
Glu Thr Arg Trp Leu Asn Glu Val Val Gly Tyr Val Ile Gly Asn Ala
```

```
          555                      560                      565
gtt ctg ggg ttt agt aca ggg tgg tgg aag gag aag cat aac ctt cat    14194
Val Leu Gly Phe Ser Thr Gly Trp Trp Lys Glu Lys His Asn Leu His
      570                      575                      580
cat gct gct cca aat gaa tgc gat cag act tac caa cca att gat gaa    14242
His Ala Ala Pro Asn Glu Cys Asp Gln Thr Tyr Gln Pro Ile Asp Glu
585                      590                      595                      600
gat att gat act ctc ccc ctc att gcc tgg agc aag gac ata ctg gcc    14290
Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp Ser Lys Asp Ile Leu Ala
                  605                      610                      615
aca gtt gag aat aag aca ttc ttg cga atc ctc caa tac cag cat ctg    14338
Thr Val Glu Asn Lys Thr Phe Leu Arg Ile Leu Gln Tyr Gln His Leu
                  620                      625                      630
ttc ttc atg ggt ctg tta ttt ttc gcc cgt ggt agt tgg ctc ttt tgg    14386
Phe Phe Met Gly Leu Leu Phe Phe Ala Arg Gly Ser Trp Leu Phe Trp
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agc tgg aga tat acc tct aca gca gtg ctc tca cct gtc gac agg ttg    14434
Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu Ser Pro Val Asp Arg Leu
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ttg gag aag gga act gtt ctg ttt cac tac ttt tgg ttc gtc ggg aca    14482
Leu Glu Lys Gly Thr Val Leu Phe His Tyr Phe Trp Phe Val Gly Thr
665                      670                      675                      680
gcg tgc tat ctt ctc cct ggt tgg aag cca tta gta tgg atg gcg gtg    14530
Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro Leu Val Trp Met Ala Val
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act gag ctc atg tcc ggc atg ctg ctg ggc ttt gta ttt gta ctt agc    14578
Thr Glu Leu Met Ser Gly Met Leu Leu Gly Phe Val Phe Val Leu Ser
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cac aat ggg atg gag gtt tat aat tcg tct aaa gaa ttc gtg agt gca    14626
His Asn Gly Met Glu Val Tyr Asn Ser Ser Lys Glu Phe Val Ser Ala
                  715                      720                      725
cag atc gta tcc aca cgg gat atc aaa gga aac ata ttc aac gac tgg    14674
Gln Ile Val Ser Thr Arg Asp Ile Lys Gly Asn Ile Phe Asn Asp Trp
                  730                      735                      740
ttc act ggt ggc ctt aac agg caa ata gag cat cat ctt ttc cca aca    14722
Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro Thr
745                      750                      755                      760
atg ccc agg cat aat tta aac aaa ata gca cct aga gtg gag gtg ttc    14770
Met Pro Arg His Asn Leu Asn Lys Ile Ala Pro Arg Val Glu Val Phe
                  765                      770                      775
tgt aag aaa cac ggt ctg gtg tac gaa gac gta tct att gct acc ggc    14818
Cys Lys Lys His Gly Leu Val Tyr Glu Asp Val Ser Ile Ala Thr Gly
                  780                      785                      790
act tgc aag gtt ttg aaa gca ttg aag gaa gtc gcg gag gct gcg gca    14866
Thr Cys Lys Val Leu Lys Ala Leu Lys Glu Val Ala Glu Ala Ala Ala
                  795                      800                      805
gag cag cat gct acc acc agt taa gctagcgtta accctgcttt aatgagatat    14920
Glu Gln His Ala Thr Thr Ser
                  810                      815
gcgagacgcc tatgatcgca tgatatttgc tttcaattct gttgtgcacg ttgtaaaaaa    14980
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cga caa cgc cag acg act gcg gta gcg aag cac aat gct gct acc ata    15862
Arg Gln Arg Gln Thr Thr Ala Val Ala Lys His Asn Ala Ala Thr Ile
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Ser Thr Gln Glu Arg Leu Cys Ser Leu Ser Ser Leu Lys Gly Glu Glu
840                 845                 850                 855
gtc tgc atc gac gga atc atc tat gac ctc caa tca ttc gat cat ccc    15958
Val Cys Ile Asp Gly Ile Ile Tyr Asp Leu Gln Ser Phe Asp His Pro
                860                 865                 870
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Gly Gly Glu Thr Ile Lys Met Phe Gly Gly Asn Asp Val Thr Val Gln
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tac aag atg att cac ccg tac cat acc gag aag cat ttg gaa aag atg    16054
Tyr Lys Met Ile His Pro Tyr His Thr Glu Lys His Leu Glu Lys Met
            890                 895                 900
aag cgt gtc ggc aag gtg acg gat ttc gtc tgc gag tac aag ttc gat    16102
Lys Arg Val Gly Lys Val Thr Asp Phe Val Cys Glu Tyr Lys Phe Asp
    905                 910                 915
acc gaa ttt gaa cgc gaa atc aaa cga gaa gtc ttc aag att gtg cga    16150
Thr Glu Phe Glu Arg Glu Ile Lys Arg Glu Val Phe Lys Ile Val Arg
920                 925                 930                 935
cga ggc aag gat ttc ggt act ttg gga tgg ttc ttc cgt gcg ttt tgc    16198
Arg Gly Lys Asp Phe Gly Thr Leu Gly Trp Phe Phe Arg Ala Phe Cys
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tac att gcc att ttc ttc tac ctg cag tac cat tgg gtc acc acg gga    16246
Tyr Ile Ala Ile Phe Phe Tyr Leu Gln Tyr His Trp Val Thr Thr Gly
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acc tct tgg ctg ctg gcc gtg gcc tac gga atc tcc caa gcg atg att    16294
Thr Ser Trp Leu Leu Ala Val Ala Tyr Gly Ile Ser Gln Ala Met Ile
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Gly Met Asn Val Gln His Asp Ala Asn His Gly Ala Thr Ser Lys Arg
    985                 990                 995
ccc tgg gtc aac gac atg cta ggc ctc ggt gcg gat ttt att ggt        16387
Pro Trp Val Asn Asp Met Leu Gly Leu Gly Ala Asp Phe Ile Gly
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Gly Ser Lys Trp Leu Trp Gln Glu Gln His Trp Thr His His Ala
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tac acc aat cac gcc gag atg gat ccc gat agc ttt ggt gcc gaa        16477
Tyr Thr Asn His Ala Glu Met Asp Pro Asp Ser Phe Gly Ala Glu
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cca atg ctc cta ttc aac gac tat ccc ttg gat cat ccc gct cgt        16522
Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp His Pro Ala Arg
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acc tgg cta cat cgc ttt caa gca ttc ttt tac atg ccc gtc ttg        16567
Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met Pro Val Leu
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Leu Gln Gln Arg Gly Ala  Leu Ser Val Gly Ile  Arg Leu Asp Asn
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Gly Leu Glu Trp Ser Trp  Arg Val Phe Gly Asn  Ile Met Leu Met
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1225              1230                1235
aaa cac ggc gtc cac tac  gcc tac tac ccg tgg  atc cac caa aac  17107
Lys His Gly Val His Tyr  Ala Tyr Tyr Pro Trp  Ile His Gln Asn
1240              1245                1250
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<211> 290

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<213> Phaeodactylum tricornutum, Physcomitrella patens

<400> 57

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Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile
        35                  40                  45
Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu
    50                  55                  60
Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu
65                  70                  75                  80
Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser
            85                  90                  95
Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr
            100                 105                 110
Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile
            115                 120                 125
Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr
    130                 135                 140
Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His
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Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His
            165                 170                 175
His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly
            180                 185                 190
Val His Val Leu Met Tyr Ala Tyr Tyr Phe Leu Ala Ala Cys Leu Arg
            195                 200                 205
Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr Leu
    210                 215                 220
Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala Tyr
225                 230                 235                 240
Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile
            245                 250                 255
Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr
            260                 265                 270
Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala Lys
            275                 280                 285
Thr Glu
    290
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<210> 58

<211> 525
<212> PRT
<213> Phaeodactylum tricornutum, Physcomitrella patens

<400> 58

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Ile Asp Val Glu His Ile Ala Ser Met Ser Leu Phe Ser Asp Phe Phe
            20                  25                  30
Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln
        35                  40                  45
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Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala
    50   55   60

Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly
65   70   75   80

Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg
              85   90   95

Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val
            100   105   110

His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr
            115   120   125

Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser
            130   135   140

Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala
145   150   155   160

Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu
            165   170   175

Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg
            180   185   190

Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr
            195   200   205

Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala
            210   215   220

Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys
225   230   235   240

Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe
            245   250   255

Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly
            260   265   270

Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys
            275   280   285

Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr
            290   295   300

Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp
305   310   315   320

Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile
            325   330   335

Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg
            340   345   350

Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu
            355   360   365

Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr
            370   375   380

Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro
385   390   395   400

Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly
            405   410   415

Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser
            420   425   430

Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly
            435   440   445

Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu
            450   455   460

His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala
465   470   475   480

Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp
            485   490   495

Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu

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<210> 59

<211> 469
<212> PRT
<213> Phaeodactylum tricornutum, Physcomitrella patens

<400> 59

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            20                  25                  30
Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr
        35                  40                  45
Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe
        50                  55                  60
Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His
65                  70                  75                  80
Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp
                85                  90                  95
Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys
            100                 105                 110
Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu
            115                 120                 125
Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu
        130                 135                 140
Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala
145                 150                 155                 160
Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala
                165                 170                 175
Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly
            180                 185                 190
Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln
            195                 200                 205
His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp
        210                 215                 220
Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp
225                 230                 235                 240
His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met
                245                 250                 255
Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile
            260                 265                 270
Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp
        275                 280                 285
Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala
        290                 295                 300
Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly
305                 310                 315                 320
Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val
                325                 330                 335
Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe
            340                 345                 350
Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu
```

```
           355                     360                     365
Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly
       370                     375                     380
Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu
385                     390                     395                     400
His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala
                   405                     410                     415
Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr
               420             · ·     425                     430
Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His
           435                     440                     445
Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro
       450                     455                     460
Leu Thr Gly Arg Ala
465
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<210> 60

<211> 26
<212> DNA
<213> unknown

<220>
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<220>
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<223> primer

<400> 60

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<210> 61

<211> 265
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<213> unknown

<220>
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<400> 61

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agcatgtgta gctcagatcc ttaccgccgg tttcggttca ttctaatgaa tatatcaccc   180
gttactatcg tattttatg aataatattc tccgttcaat ttactgattg tccgtcgacg   240
aattcgagct cggcgcgcca agctt                                         265
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<210> 62

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<212>  DNA
<213>  unknown

<220>
<223>  primer

<220>
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<222>  (1)..(257)
<223>  primer

<400>  62

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tgatcgcatg atatttgctt tcaattctgt tgtgcacgtt gtaaaaaacc tgagcatgtg     120
tagctcagat ccttaccgcc ggtttcggtt cattctaatg aatatatcac ccgttactat     180
cgtattttta tgaataatat tctccgttca atttactgat tgtccgtcga cgaattcgag     240
ctcggcgcgc caagctt                                                     257


<210>  63

<211>  5410
<212>  DNA
<213>  unknown

<220>
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<220>
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<223>  Plant expression vector

<400>  63

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ggattttgca atactttcat tcatacacac tcactaagtt ttacacgatt ataatttctt     180
catagccagc ggatccgata tcgggcccgc tagcgttaac cctgctttaa tgagatatgc     240
gagacgccta tgatcgcatg atatttgctt tcaattctgt tgtgcacgtt gtaaaaaacc     300
tgagcatgtg tagctcagat ccttaccgcc ggtttcggtt cattctaatg aatatatcac     360
ccgttactat cgtattttta tgaataatat tctccgttca atttactgat tgtccgtcga     420
gcaaatttac acattgccac taaacgtcta aacccttgta atttgttttt gttttactat     480
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tttttgtctt ctaaatacat atactaatca actggaaatg taaatatttg ctaatatttc     660
tactatagga gaattaaagt gagtgaatat ggtaccacaa ggtttggaga tttaattgtt     720
gcaatgctgc atggatggca tatacaccaa acattcaata attcttgagg ataataatgg     780
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<211> 12093
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<400> 64

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Glu Asp Ala Trp Ile Ile His Ser Asn Lys Val Tyr Asp Val Ser Asn
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tgg cac gaa cat ccc gga ggc gcc gtc att ttc acg cac gcc ggt gac      194
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Asp Met Thr Asp Ile Phe Ala Ala Phe His Ala Pro Gly Ser Gln Ser
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    80                  85                  90
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Lys Glu Pro Gln Gln Ile Ala Phe Glu Lys Gly Tyr Arg Asp Leu Arg
95                  100                 105                 110
tcc aaa ctc atc atg atg ggc atg ttc aag tcc aac aag tgg ttc tac      386
Ser Lys Leu Ile Met Met Gly Met Phe Lys Ser Asn Lys Trp Phe Tyr
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gtc tac aag tgc ctc agc aac atg gcc att tgg gcc gcc gcc tgt gct      434
Val Tyr Lys Cys Leu Ser Asn Met Ala Ile Trp Ala Ala Ala Cys Ala
            130                 135                 140
ctc gtc ttt tac tcg gac cgc ttc tgg gta cac ctg gcc agc gcc gtc      482
Leu Val Phe Tyr Ser Asp Arg Phe Trp Val His Leu Ala Ser Ala Val
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Leu His His Gln Val Phe Thr Lys Arg Lys His Gly Asp Leu Gly Gly
175                 180                 185                 190
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Phe Tyr Phe Pro Ile Leu Leu Leu Ala Arg Leu Ser Trp Leu Asn Glu
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His Leu Phe Pro Ser Leu Pro Arg His Asn Leu Ala Lys Thr His Ala
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Asp Leu Val Asp Gly Thr Met Glu Val Leu His His Leu Gly Ser Val
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<213> Phaeodactylum tricornutum

<400> 70

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Thr Asp Ile Phe Ala Ala Phe His Ala Pro Gly Ser Gln Ser Leu Met
65                  70                  75                  80
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Pro Gln Gln Ile Ala Phe Glu Lys Gly Tyr Arg Asp Leu Arg Ser Lys
            100                 105                 110
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Lys Cys Leu Ser Asn Met Ala Ile Trp Ala Ala Ala Cys Ala Leu Val
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145                 .150                150 155                 160
Gly Thr Phe Phe Gln Gln Ser Gly Trp Leu Ala His Asp Phe Leu His
                165                 170                 175
His Gln Val Phe Thr Lys Arg Lys His Gly Asp Leu Gly Gly Leu Phe
            180                 185                 190
Trp Gly Asn Leu Met Gln Gly Tyr Ser Val Gln Trp Trp Lys Asn Lys
            195                 200                 205
His Asn Gly His His Ala Val Pro Asn Leu His Cys Ser Ser Ala Val
        210                 215                 220
Ala Gln Asp Gly Asp Pro Asp Ile Asp Thr Met Pro Leu Leu Ala Trp
225                 230                 235                 240
Ser Val Gln Gln Ala Gln Ser Tyr Arg Glu Leu Gln Ala Asp Gly Lys
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Asp Ser Gly Leu Val Lys Phe Met Ile Arg Asn Gln Ser Tyr Phe Tyr
            260                 265                 270
Phe Pro Ile Leu Leu Leu Ala Arg Leu Ser Trp Leu Asn Glu Ser Phe
            275                 280                 285
Lys Cys Ala Phe Gly Leu Gly Ala Ala Ser Glu Asn Ala Ala Leu Glu
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Leu Lys Ala Lys Gly Leu Gln Tyr Pro Leu Leu Glu Lys Ala Gly Ile
305                 310                 315                 320
Leu Leu His Tyr Ala Trp Met Leu Thr Val Ser Ser Gly Phe Gly Arg
                325                 330                 335
Phe Ser Phe Ala Tyr Thr Ala Phe Tyr Phe Leu Thr Ala Thr Ala Ser
            340                 345                 350
Cys Gly Phe Leu Leu Ala Ile Val Phe Gly Leu Gly His Asn Gly Met
        355                 360                 365
Ala Thr Tyr Asn Ala Asp Ala Arg Pro Asp Phe Trp Lys Leu Gln Val
        370                 375                 380
Thr Thr Thr Arg Asn Val Thr Gly Gly His Gly Phe Pro Gln Ala Phe
385                 390                 395                 400
Val Asp Trp Phe Cys Gly Gly Leu Gln Tyr Gln Val Asp His His Leu
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Phe Pro Ser Leu Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val
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              420                      425                      430
Glu Ser Phe Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu
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tatttggtac taaatttata acacctttta tgctaacgtt gccaacact tagcaatttg      480
caagttgatt aattgattct aaattatttt tgtcttctaa atacatatac taatcaactg     540
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gccgc atg gag gtc gtg gag aga ttc tac ggt gag ttg gat ggg aag gtc    1070
      Met Glu Val Val Glu Arg Phe Tyr Gly Glu Leu Asp Gly Lys Val
        1                   5                  10                  15
tcg cag ggc gtg aat gca ttg ctg ggt agt ttt ggg gtg gag ttg acg    1118
Ser Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr
              20                      25                      30
gat acg ccc act acc aaa ggc ttg ccc ctc gtt gac agt ccc aca ccc    1166
Asp Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro
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atc gtc ctc ggt gtt tct gta tac ttg act att gtc att gga ggg ctt    1214
Ile Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu
                50                          55                          60
ttg tgg ata aag gcc agg gat ctg aaa ccg cgc gcc tcg gag cca ttt    1262
Leu Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe
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ttg ctc caa gct ttg gtg ctt gtg cac aac ctg ttc tgt ttt gcg ctc    1310
Leu Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu
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agt ctg tat atg tgc gtg ggc atc gct tat cag gct att acc tgg cgg    1358
Ser Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg
                        100                         105                         110
tac tct ctc tgg ggc aat gca tac aat cct aaa cat aaa gag atg gcg    1406
Tyr Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala
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att ctg gta tac ttg ttc tac atg tct aag tac gtg gaa ttc atg gat    1454
Ile Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp
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acc gtt atc atg ata ctg aag cgc agc acc agg caa ata agc ttc ctc    1502
Thr Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu
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cac gtt tat cat cat tct tca att tcc ctc att tgg tgg gct att gct    1550
His Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala
160                         165                         170                         175
cat cac gct cct ggc ggt gaa gca tat tgg tct gcg gct ctg aac tca    1598
His His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser
                        180                         185                         190
gga gtg cat gtt ctc atg tat gcg tat tac ttc ttg gct gcc tgc ctt    1646
Gly Val His Val Leu Met Tyr Ala Tyr Tyr Phe Leu Ala Ala Cys Leu
                195                         200                         205
cga agt agc cca aag tta aaa aat aag tac ctt ttt tgg ggc agg tac    1694
Arg Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr
                210                         215                         220
ttg aca caa ttc caa atg ttc cag ttt atg ctg aac tta gtg cag gct    1742
Leu Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala
        225                         230                         235
tac tac gac atg aaa acg aat gcg cca tat cca caa tgg ctg atc aag    1790
Tyr Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys
240                         245                         250                         255
att ttg ttc tac tac atg atc tcg ttg ctg ttt ctt ttc ggc aat ttt    1838
Ile Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe
                        260                         265                         270
tac gta caa aaa tac atc aaa ccc tct gac gga aag caa aag gga gct    1886
Tyr Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala
                275                         280                         285
aaa act gag tga tctagaaggc ctcctgcttt aatgagatat gcgagacgcc    1938
Lys Thr Glu
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tcatagccag cggatccgcc cacata atg gag aac ttc tgg tct att gtt gtg     2831
                               Met Glu Asn Phe Trp Ser Ile Val Val
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ttt ttt cta ctc tca att ctc ttc att tta tat aac ata tcg aca gta    2879
Phe Phe Leu Leu Ser Ile Leu Phe Ile Leu Tyr Asn Ile Ser Thr Val
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tgc cac tac tat atg cgg att tcg ttt tat tac ttc aca att tta ttg    2927
Cys His Tyr Tyr Met Arg Ile Ser Phe Tyr Tyr Phe Thr Ile Leu Leu
                320                 325                 330
cat gga atg gaa gtt tgt gtt aca atg atc cct tct tgg cta aat ggg    2975
His Gly Met Glu Val Cys Val Thr Met Ile Pro Ser Trp Leu Asn Gly
            335                 340                 345
aag ggt gct gat tac gtg ttt cac tcg ttt ttc tat tgg tgt aaa tgg    3023
Lys Gly Ala Asp Tyr Val Phe His Ser Phe Phe Tyr Trp Cys Lys Trp
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act ggt gtt cat aca aca gtc tat gga tat gaa aaa aca caa gtt gaa    3071
Thr Gly Val His Thr Thr Val Tyr Gly Tyr Glu Lys Thr Gln Val Glu
        365                 370                 375
ggt ccg gct gta gtt att tgt aat cat cag agt tct ctc gac att cta    3119
Gly Pro Ala Val Val Ile Cys Asn His Gln Ser Ser Leu Asp Ile Leu
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tcg atg gca tca atc tgg ccg aag aat tgt gtt gta atg atg aaa cga    3167
Ser Met Ala Ser Ile Trp Pro Lys Asn Cys Val Val Met Met Lys Arg
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att ctt gcc tat gtt cca ttc ttc aat ctc gga gcc tac ttt tcc aac    3215
Ile Leu Ala Tyr Val Pro Phe Phe Asn Leu Gly Ala Tyr Phe Ser Asn
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aca atc ttc atc gat cga tat aac cgt gaa cgt gcg atg gct tca gtt    3263
Thr Ile Phe Ile Asp Arg Tyr Asn Arg Glu Arg Ala Met Ala Ser Val
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Asp Tyr Cys Ala Ser Glu Met Lys Asn Arg Asn Leu Lys Leu Trp Val
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Phe Pro Glu Gly Thr Arg Asn Arg Glu Gly Gly Phe Ile Pro Phe Lys
460                 465                 470                 475
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Lys Gly Ala Phe Asn Ile Ala Val Arg Ala Gln Ile Pro Ile Ile Pro
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Val Val Phe Ser Asp Tyr Arg Asp Phe Tyr Ser Lys Pro Gly Arg Tyr
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aca aaa ggg ctc act ctt gat gac gtc agc gag ttg tct gat atg tgt    3551
Thr Lys Gly Leu Thr Leu Asp Asp Val Ser Glu Leu Ser Asp Met Cys
        525                 530                 535
cgg gac gtt atg ttg gca gcc tat aag gaa gtt act cta gaa gct cag    3599
Arg Asp Val Met Leu Ala Ala Tyr Lys Glu Val Thr Leu Glu Ala Gln
540                 545                 550                 555
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Glu

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acg gcg gct cgc aag atc agt tgg cag gaa gtc aag acc cac gcg tct       4640
Thr Ala Ala Arg Lys Ile Ser Trp Gln Glu Val Lys Thr His Ala Ser
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ccg gag gac gcc tgg atc att cac tcc aat aag gtc tac gac gtg tcc       4688
Pro Glu Asp Ala Trp Ile Ile His Ser Asn Lys Val Tyr Asp Val Ser
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aac tgg cac gaa cat ccc gga ggc gcc gtc att ttc acg cac gcc ggt       4736
Asn Trp His Glu His Pro Gly Gly Ala Val Ile Phe Thr His Ala Gly
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gac gac atg acg gac att ttc gct gcc ttt cac gca ccc gga tcg cag       4784
Asp Asp Met Thr Asp Ile Phe Ala Ala Phe His Ala Pro Gly Ser Gln
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Ser Leu Met Lys Lys Phe Tyr Ile Gly Glu Leu Leu Pro Glu Thr Thr
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Gly Lys Glu Pro Gln Gln Ile Ala Phe Glu Lys Gly Tyr Arg Asp Leu
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Arg Ser Lys Leu Ile Met Met Gly Met Phe Lys Ser Asn Lys Trp Phe
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Ala Leu Val Phe Tyr Ser Asp Arg Phe Trp Val His Leu Ala Ser Ala
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Val Met Leu Gly Thr Phe Phe Gln Gln Ser Gly Trp Leu Ala His Asp
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Phe Leu His His Gln Val Phe Thr Lys Arg Lys His Gly Asp Leu Gly·
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Lys Asn Lys His Asn Gly His His Ala Val Pro Asn Leu His Cys Ser
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Ser Ala Val Ala Gln Asp Gly Asp Pro Asp Ile Asp Thr Met Pro Leu
    795                 800                 805
ctc gcc tgg tcc gtc cag caa gcc cag tct tac cgg gaa ctc caa gcc        5312
Leu Ala Trp Ser Val Gln Gln Ala Gln Ser Tyr Arg Glu Leu Gln Ala
810.                815                 820                 825
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Asp Gly Lys Asp Ser Gly Leu Val Lys Phe Met Ile Arg Asn Gln Ser
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Glu Ser Phe Lys Cys Ala Phe Gly Leu Gly Ala Ala Ser Glu Asn Ala
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Ala Leu Glu Leu Lys Ala Lys Gly Leu Gln Tyr Pro Leu Leu Glu Lys
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Ala Gly Ile Leu Leu His Tyr Ala Trp Met Leu Thr Val Ser Ser Gly
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Leu Gln Val Thr Thr Thr Arg Asn Val Thr Gly Gly His Gly Phe Pro
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Gln Ala Phe Val Asp Trp Phe Cys Gly Gly Leu Gln Tyr Gln Val Asp
970                 975                 980                 985
cac cac tta ttc ccc agc ctg ccc cga cac aat ctg gcc aag aca   cac      5840
His His Leu Phe Pro Ser Leu Pro Arg His Asn Leu Ala Lys Thr   His
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Ala Leu Val Glu  Ser Phe Cys Lys Glu  Trp Gly Val Gln Tyr   His
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Glu Ala Asp Leu  Val Asp Gly Thr Met  Glu Val Leu His His   Leu
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<211> 290
<212> PRT
<213> Phaeodactylum tricornutum, Physcomitrella patens, Caenorhabditis elegans

<400> 72

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Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile
        35                  40                  45
Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu
    50                  55                  60
Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu
65                  70                  75                  80
Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser
            85                  90                  95
Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr
            100                 105                 110
Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile
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Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr
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Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His
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Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His
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His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly
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Val His Val Leu Met Tyr Ala Tyr Tyr Phe Leu Ala Ala Cys Leu Arg
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Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr Leu
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Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala Tyr
225                 230                 235                 240
Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile
                245                 250                 255
Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr
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Thr Glu
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<211>   282
<212>   PRT
<213>   Phaeodactylum tricornutum, Physcomitrella patens, Caenorhabditis elegans

<400>   73

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Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
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Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
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His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val
65   70   75   80
Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys
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Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro
            100   105   110
Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe
            115   120   125
Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr
    130   135   140
Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met
145   150   155   160
Lys Asn Arg Asn Leu Lys Leu Trp Val Phe Pro Glu Gly Thr Arg Asn
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Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala
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Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp
225   230   235   240
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Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu
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<211>   477
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<213>   Phaeodactylum tricornutum, Physcomitrella patens, Caenorhabditis elegans

<400>   74

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        35                      40                      45
Glu His Pro Gly Gly Ala Val Ile Phe Thr His Ala Gly Asp Asp Met
        50                      55                      60
Thr Asp Ile Phe Ala Ala Phe His Ala Pro Gly Ser Gln Ser Leu Met
65                      70                      75                      80
Lys Lys Phe Tyr Ile Gly Glu Leu Leu Pro Glu Thr Thr Gly Lys Glu
                85                      90                      95
Pro Gln Gln Ile Ala Phe Glu Lys Gly Tyr Arg Asp Leu Arg Ser Lys
            100                     105                     110
Leu Ile Met Met Gly Met Phe Lys Ser Asn Lys Trp Phe Tyr Val Tyr
            115                     120                     125
Lys Cys Leu Ser Asn Met Ala Ile Trp Ala Ala Ala Cys Ala Leu Val
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Phe Tyr Ser Asp Arg Phe Trp Val His Leu Ala Ser Ala Val Met Leu
145                     150                     155                     160
Gly Thr Phe Phe Gln Gln Ser Gly Trp Leu Ala His Asp Phe Leu His
                165                     170                     175
His Gln Val Phe Thr Lys Arg Lys His Gly Asp Leu Gly Gly Leu Phe
            180                     185                     190
Trp Gly Asn Leu Met Gln Gly Tyr Ser Val Gln Trp Trp Lys Asn Lys
            195                     200                     205
His Asn Gly His His Ala Val Pro Asn Leu His Cys Ser Ser Ala Val
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Ala Gln Asp Gly Asp Pro Asp Ile Asp Thr Met Pro Leu Leu Ala Trp
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Asp Ser Gly Leu Val Lys Phe Met Ile Arg Asn Gln Ser Tyr Phe Tyr
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Phe Pro Ile Leu Leu Leu Ala Arg Leu Ser Trp Leu Asn Glu Ser Phe
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Phe Ser Phe Ala Tyr Thr Ala Phe Tyr Phe Leu Thr Ala Thr Ala Ser
            340                     345                     350
Cys Gly Phe Leu Leu Ala Ile Val Phe Gly Leu Gly His Asn Gly Met
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Ala Thr Tyr Asn Ala Asp Ala Arg Pro Asp Phe Trp Lys Leu Gln Val
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385                     390                     395                     400
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Phe Pro Ser Leu Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val
            420                     425                     430
Glu Ser Phe Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu
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<400> 76
ccggaattcg gcgcgccgag ctcctcgagc aaatttacac attgcca   47

<210> 77
<211> 47
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(47)
<223> USP3 upstream

<400> 77
ccggaattcg gcgcgccgag ctcctcgagc aaatttacac attgcca   47

<210> 78
<211> 48
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(48)

<223> USP1 downstream

<400> 78
aaaactgcag gcggccgccc accgcggtgg gctggctatg aagaaatt   48

<210> 79
<211> 27
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(27)
<223> USP2 downstream

<400> 79
cgcggatccg ctggctatga agaaatt   27

<210> 80
<211> 45
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(45)
<223> USP3 downstream

<400> 80
tcccccggga tcgatgccgg cagatctgct ggctatgaag aaatt   45

<210> 81
<211> 40
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(40)
<223> OCS1 upstream

<400> 81
aaaactgcag tctagaaggc ctcctgcttt aatgagatat   40

<210> 82
<211> 51
<212> DNA
<213> unknown

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<220>
<221>  misc_feature
<222>  (1)..(51)
<223>  OCS2 upstream

<400>  82
cgcggatccg atatcgggcc cgctagcgtt aaccctgctt taatgagata t          51


<210>  83
<211>  33
<212>  DNA
<213>  unknown


<220>
<221>  misc_feature
<222>  (1)..(33)
<223>  OCS3 upstream

<400>  83
tcccccgggc catggcctgc tttaatgaga tat                              33


<210>  84
<211>  53
<212>  DNA
<213>  unknown


<220>
<221>  misc_feature
<222>  (1)..(53)
<223>  OCS1 downstream

<400>  84
cccaagcttg gcgcgccgag ctcgaattcg tcgacggaca atcagtaaat tga        53


<210>  85
<211>  53
<212>  DNA
<213>  unknown


<220>
<221>  misc_feature
<222>  (1)..(53)
<223>  OCS2 downstream

<400>  85
cccaagcttg gcgcgccgag ctcgaattcg tcgacggaca atcagtaaat tga        53


<210>  86
<211>  47
<212>  DNA
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<213>   unknown

<220>
<221>   misc_feature
<222>   (1)..(47)
<223>   OCS3 downstream

<400>   86
cccaagcttg gcgcgccgag ctcgtcgacg gacaatcagt aaattga   47

<210>   87
<211>   29
<212>   DNA
<213>   unknown

<220>
<221>   misc_feature
<222>   (1)..(29)
<223>   5 T06E8.1f

<400>   87
acataatgga gaacttctgg tcgatcgtc   29

<210>   88
<211>   24
<212>   DNA
<213>   unknown

<220>
<221>   misc_feature
<222>   (1)..(24)
<223>   3 T06E8.1r

<400>   88
ttactcagat ttcttcccgt cttt   24

<210>   89
<211>   26
<212>   DNA
<213>   unknown

<220>
<221>   misc_feature
<222>   (1)..(26)
<223>   5 F59F4.4f

<400>   89
acataatgac cttcctagcc atatta   26

<210> 90
<211> 24
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(24)
<223> 3 F59F4.4r

<400> 90
tcagatattc aaattggcgg cttc   24

<210> 91
<211> 32
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(32)
<223> ARe503f

<400> 91
ttaagcgcgg ccgcatggag aacttctggt cg   32

<210> 92
<211> 31
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(31)
<223> ARe504r

<400> 92
acctcggcgg ccgccctttt actcagattt c   31

<210> 93
<211> 41
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(41)
<223> Forward primer

<400> 93

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acataatgga gaacttctgg tctattgttg tgttttttct a                    41
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<210> 94
<211> 41
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(41)
<223> Reverse primer

<400> 94
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ctagctagct tactcagatt tcttcccgtc ttttgtttct c                    41
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<210> 95
<211> 18
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(18)
<223> primer

<400> 95
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caggaaacag ctatgacc                                              18
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<210> 96
<211> 19
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(19)
<223> primer

<400> 96
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ctaaagggaa caaaagctg                                             19
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<210> 97
<211> 18
<212> DNA
<213> unknown

<220>
<221> misc_feature

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<222>  (1)..(18)
<223>  primer

<400>  97
tgtaaaacga cggccagt                                        18


<210>  98
<211>  18
<212>  DNA
<213>  unknown


<220>
<221>  misc_feature
<222>  (1)..(18)
<223>  LPAAT069-5

<400>  98
gctacattgc catggagc                                        18


<210>  99
<211>  19
<212>  DNA
<213>  unknown


<220>
<221>  misc_feature
<222>  (1)..(19)
<223>  LPAAT069-3

<400>  99
gctacaagag gtcaggtcg                                       19


<210>  100
<211>  25
<212>  DNA
<213>  unknown


<220>
<221>  misc_feature
<222>  (1)..(25)
<223>  ACtrau-5

<400>  100
ctggatccat gagcgcgtgg acgag                                25


<210>  101
<211>  25
<212>  DNA
<213>  unknown
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<220>
<221> misc_feature
<222> (1)..(25)
<223> ACtrau-3

<400> 101
ttggatccca agaggtcagg tcgga   25

<210> 102
<211> 26
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(26)
<223> ACtrau-3 stop

<400> 102
ttggatccct acaagaggtc aggtcg   26

<210> 103
<211> 22
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(22)
<223> YES-HIS-5

<400> 103
ctgagctcat gagcgcgtgg ag   22

<210> 104
<211> 35
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(35)
<223> YES-HIS-3

<400> 104
atggatccgt gatggtgatg gtgatgcaag aggtc   35

<210> 105
<211> 18

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<212>   DNA
<213>   unknown


<220>
<221>   misc_feature
<222>   (1)..(18)
<223>   LPAAT069-5

<400>   105
gctacattgc catggagc                                                    18


<210>   106
<211>   19
<212>   DNA
<213>   unknown


<220>
<221>   misc_feature
<222>   (1)..(19)
<223>   LPAAT069-3

<400>   106
gctacaagag gtcaggtcg                                                   19


<210>   107
<211>   41
<212>   DNA
<213>   unknown

<220>
<223>   primer


<220>
<221>   misc_feature
<222>   (1)..(41)
<223>   MaLPAAT1.1

<400>   107
atggatgaat ccaccacgac catcagcccg atgcttgctg c                          41


<210>   108
<211>   40
<212>   DNA
<213>   unknown


<220>
<221>   misc_feature
<222>   (1)..(40)
<223>   MaLPAAT1.2
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<400> 108
atgaaccota tctacaaggg ttcagcccga tgcttgctgc   40

<210> 109
<211> 37
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(37)
<223> ShLPAAT

<400> 109
atgttactgc tagcatttgt ttactttgcc attaagg   37

<210> 110
<211> 46
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(46)
<223> T6

<400> 110
atgagcgcgt ggacgagggc ctacaagagg tcaggtcgga cgtaca   46

<210> 111
<211> 40
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(40)
<223> Pp00406404

<400> 111
atggctttga tgtatatctg ttacacgatt tttctttag   40

<210> 112
<211> 41
<212> DNA
<213> unknown

<220>
<221> misc_feature

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<222>    (1)..(41)
<223>    Pp02006422

<400>    112
atgctgatat tacagcccctt cctaatgaac aggaagaccg t                    41


<210>    113
<211>    39
<212>    DNA
<213>    unknown


<220>
<221>    misc_feature
<222>    (1)..(39)
<223>    Pp01505214

<400>    113
atgatccgga ttttcagagt cagtccgttt tgccgaggt                        39


<210>    114
<211>    39
<212>    DNA
<213>    unknown


<220>
<221>    misc_feature
<222>    (1)..(39)
<223>    Pp00403422

<400>    114
atgccgtcgc tgtttcgggt caatcagttc gcctgcttc                        39


<210>    115
<211>    41
<212>    DNA
<213>    unknown


<220>
<221>    misc_feature
<222>    (1)..(41)
<223>    Pp00410427

<400>    115
atgctgatat tacagcccctt cctaatgaac aggaagaccg t                    41


<210>    116
<211>    39
<212>    DNA
<213>    unknown
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<220>
<221>  misc_feature
<222>  (1)..(39)
<223>  Pp02001815

<400>  116
atgaccagca cggaaaatac ctagatgtta gtttcactc                              39


<210>  117
<211>  40
<212>  DNA
<213>  unknown


<220>
<221>  misc_feature
<222>  (1)..(40)
<223>  Pp01503434

<400>  117
atgattatga tggaggtgct gtcagtccgt tttgccgagg                             40


<210>  118
<211>  40
<212>  DNA
<213>  unknown


<220>
<221>  misc_feature
<222>  (1)..(40)
<223>  Pp01503336

<400>  118
atgtgttcaa tttcttgtgg ttagtggaac ataagctgtt                             40


<210>  119
<211>  41
<212>  DNA
<213>  unknown


<220>
<221>  misc_feature
<222>  (1)..(41)
<223>  Fg003028298

<400>  119
atgggaaagt ccactttacc tatgaagtct cctcatcatc g                           41


<210>  120
<211>  27
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<212>  DNA
<213>  unknown


<220>
<221>  misc_feature
<222>  (1)..(27)
<223>  GSP

<400>  120
tctctttttc gtgctgctcc agccgat                                    27


<210>  121
<211>  52
<212>  DNA
<213>  unknown

<220>
<223>  primer


<220>
<221>  misc_feature
<222>  (1)..(52)
<223>  5 primer att1ThLPAAT

<400>  121
ggggacaagt ttgtacaaaa aagcaggctc catgagcgcg tggacgaggg cc        52


<210>  122
<211>  72
<212>  DNA
<213>  unknown


<220>
<221>  misc_feature
<222>  (1)..(72)
<223>  3 primer att2ThLPAAT

<400>  122
ggggaccact ttgtacaaga aagctgggtc tagtggtggt ggtggtggtg caagaggtca    60

ggtcggacgt ac                                                    72
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